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October 30, 2004, 01:28:51; Search time 154 Seconds (without alignments) 444.918 Million cell updates/sec
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 version 5.1.6
- 2004 Compugen Ltd.
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Listing first 45 summaries
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1 MSTLPKPQRKTKRNTNRRPT...
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:*

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Database :

STIMMARTES

	Description	Aar92987 Hepatitis	Aar92972 Hepatitis	Aar92974 Hepatitis	Aar92973 Hepatitis	m	Aar92978 Hepatitis	9	Aar92977 Hepatitis	Aar74048 Synthetic	Aar74047 Synthetic	9		Aar38278 NANB hepa	Aar24440 Composite	Aar70230 Composite	Aar66995 Hepatitis	Aar44010 Hepatitis	Aar92938 Hepatitis	Aar92941 Hepatitis	Aar92937 Hepatitis	Aar92939 Hepatitis	Aar92940 Hepatitis	Aay94411 Human hep	Adj10436 HCV Core	Adj10438 HCV Core(
SUMMARIES	ID	AAR92987	AAR92972	AAR92974	AAR92973	AAR92953	AAR92978	AAR92976	AAR92977	AAR74048	AAR74047	AAR96546	AAR22137	AAR38278	AAR24440	AAR70230	AAR66995	AAR44010	AAR92938	AAR92941	AAR92937	AAR92939	AAR92940	AAY94411	ADJ10436	ADJ10438
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ALIGNMENTS

AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV in serum, saliva, lymphocytes or be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection. HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine; hepatitis. Hepatitis C virus isolate HK2 core protein. AAR92987 standard; protein; 191 AA. Claim 4; Page 223; 340pp; English. Purcell RH; 95WO-US010398. 94US-00290665. (USSH) US SEC DEPT HEALTH. (first entry) WPI; 1996-139709/14. Bukh J, Miller RH, Hepatitis C virus. Sequence 191 AA; N-PSDB; AAT16661 HCV infection WO9605315-A2. 15-AUG-1995; 15-AUG-1994; 02-OCT-1996 22-FEB-1996. AAR92987; RESULT 1 AAR92987

Length 191; 100.0%; Score 1045; DB 2; 100.0%; Pred. No. 2.5e-90; Query Match Best Local Similarity RROPI PKAROPOGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG

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                                                                          61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                MSTLPKPQRKTKRNTNRRPTDVKFPGGQ1VGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                          RROPIPKARQPOGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                                                                                  KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYAIGNLPGCSFSIFLLA
                                                                                                                   KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
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Mismatches
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Best Local Simi
Matches 181;
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determine HCV genotype and as vaccines against HCV infection
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Matches 179; Conservative
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Pred. No. 2.1e-84;
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93.7%;
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                                                                                                                                                                                                                                                      (first entry)
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                                      LLSCLTTPASA 191
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                                                          Miller RH,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-AUG-1995;
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                                                                                                                                                                                                                                                      02-OCT-1996
                                                                                                                                                                                                                                                                                                                             HCV; E1; e.
hepatitis.
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Matches 179;
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121
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AARSO 73
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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV insertum. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRQPIPKARQPEGRTWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLG 120
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                                                                                                                                                                                                                  envelope 1; core protein; HCV genotyping; antibody; vaccine;
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Pred. No. 2.6e-84;
5; Mismatches 7; Indels
                                                                                                                                                             Hepatitis C virus isolate HK3 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 194-195; 340pp; English.
  A.
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AAR92953 standard; protein; 191
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93.7%;
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                                                                                                          (first entry)
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N-PSDB; AAT16627.
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Best Local Similarity
                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-AUG-1995;
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                                                                                                          02-OCT-1996
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                                                                                                                                                                                                               HCV; E1; en
hepatitis.
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(USSH ) US SEC
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                                                                             15-AUG-1995;
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hepatitis.
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                                                                                                                                        Bukh J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                   DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
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                                                envelope 1; core protein; HCV genotyping; antibody; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                Score 980; DB 2; I
Pred. No. 3.3e-84;
4; Mismatches 8;
                            Hepatitis C vírus isolate DK13 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus isolate 26 core protein.
                                                                                                                                                                                                                                                                                Claim 4; Page 215-216; 340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR92976 standard; protein; 191 AA.
                                                                                                                                                                                                   RH;
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                                                                                                                                        95WO-US010398
                                                                                                                                                           94US-00290665
                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%;
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         (first entry
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Best Local Similarity 93.7
Matches 179; Conservative
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                                                                                                                                                                                                                     WPI; 1996-139709/14.
N-PSDB; AAT16652.
                                                                                                                                                                                                  Miller RH,
                                                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                          HCV infection
                                                                                                                                        15-AUG-1995;
                                                                                                                                                            15-AUG-1994;
                                                                                                 WO9605315-A2
        02-OCT-1996
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                                                            hepatitis.
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                                                E1;
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                                                HCV;
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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated CDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monounclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
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Pred. No. 5.1e-84;
5; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                             Purcell RH;
                                                                                                                                                                                        95WO-US010398
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93.2%;
                                                                                                                                                                                                                                                                                                               DEPT HEALTH
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Best Local Similarity 93.2
Matches 178; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-139709/14
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT16650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 191 AA;
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09 9 120 120 180

DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection. Claim 4; Page 214-215; 340pp; English Purcell RH; Miller RH, 1996-139709/14 N-PSDB; AAT16651 Bukh J,

isolates. Isolated CDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of AAR92936-R92987 are HCV core proteins derived from 52 different

Sequence 191 AA;

ö RROPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120 120 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180 9 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG Gaps .; 0 93.5%; Score 977; DB 2; Length 191; 93.2%; Pred. No. 6.3e-84; 8; Indels 5; Mismatches Matches 178; Conservative LLSCLTTPASA 191 LLSCLTVPASA 191 Best Local Similarity 61 61 121 121 181 Query Match 181 à g ₽ d à g δ 셤

RESULT 9

AAR74048 standard; protein; 196 AA. nucleocapsid protein. (revised)
(first entry) Synthetic HCV 25-MAR-2003 26-NOV-1995 AAR74048;

Hepatitis C virus; vector; expression; prokaryotic cells; detection; diagnosis.

Synthetic

WO9511980-A2

04-MAY-1995

94WO-US012166 25-OCT-1994;

93US-00141917 25-OCT-1993;

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The sequence is that of a synthetic nucleotide sequence encoding the hepatitis C virus nucleocapsid protein. The gene is positioned in a vector for efficient expression in prokaryotic cells. The expressed protein can be used in tests for the detection of antibodies specific for the HCV C protein. See also AAR74047. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                        Vector for expression of a synthetically produced protein coding DNA - pref. encodes the hepatitis C virus nucleo-capsid protein which can be used in the detection of HCV antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RROPIPKAROPOGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRQPIPKVRRPEGRIWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPIDPRRRSRNLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                93.5%; Score 977; DB 2; Le
92.1%; Pred. No. 6.5e-84;
Mismatches 9;
               (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                    Disclosure; Page 37; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 92.1
Matches 176; Conservative
                                                   Khudyakov Y, Fields HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LLSCLTVPASA 191
                                                                                       1995-178872/23
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                          N-PSDB; AAQ92071
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 196 AA;
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09 9 180

120 120

> AAR74047 standard; protein; 196 AA. (revised)
> (first entry) 25-MAR-2003 26-NOV-1995 AAR74047; RESULT 10 AAR74047

Synthetic HCV nucleocapsid protein.

Hepatitis C virus; vector; expression; prokaryotic cells; detection; diagnosis.

Synthetic.

WO9511980-A2

04-MAY-1995.

94WO-US012166. 25-OCT-1994;

93US-00141917. 25-OCT-1993;

(USSH) US DEPT HEALTH & HUMAN SERVICES

Fields HA; Khudyakov Y,

WPI; 1995-178872/23

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the partities C virus subtypes different from subtypes 1a-c, 2a-d, 3a-f, 4a-f, 5a and 6a. They esp. from the novel subtypes 1a-c, 2a-d, 3a-f, 3a-f, 4a-d, 5a and 6a. They esp. from the novel subtypes 1a-c, 2a-d, 3a-f, 3a-f, 4a-m, 7a-cor types 9, 10 or 11. The sequences corresp. to the 5' untranslated region (WR), the Core/E1, NG4 or NS5B regions of the genome. This sequence represents amino acids 1-317 from the HCV types 9a and 7a isolates RR1. The new HCV types were isolated from patients with chronic HCV from the Benelux countries, France, Cameroon and Vietnam, because of their aberrant reactivities. The RNA was extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The 5'UR, Core/E1 and NSSB regions over sequenced either directly or partially and used to classify the new viruses into (sub) types based on comparison with known sequences. The sequences were used to generate the peptides ARR96424-R86524. The sequences can also be used to synthesise probes and primers for the detection of HCV in a sample. The polypeptides can be used to detect anticed the detections of HCV typing or to prevent HCV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KVIDTLTXXLADIMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; non-A non-B virus; HCV-Hc59; antigen; vaccine; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSTLPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                                                                                                                                                                                                                                                                                                                    The sequences AAR96526-R96578 represent novel sequences isolated from
                                                                                                                                                                                Hepatitis C virus poly:nucleic acid unique to unidentified sub:type used to develop probes and primers for new sub:types and vaccines to prevent and treat infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.5%; Score 977; DB 2; Length 31 93.7%; Pred. No. 1.1e-83; ive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV-Hc59 capsid and envelope proteins.
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                                                                                                                                                                                                                                                                              Claim 25; Fig 3; 150pp; English.
95EP-00870076.
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Best Local Similarity 93.7
Matches 179; Conservative
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                                        (INNO-) INNOGENETICS NV.
                                                                                  Stuyver L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-A.
non-B hepatitis virus.
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                                                                                                                           WPI; 1996-251460/25.
N-PSDB; AAT27957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 319 AA;
28-JUN-1995;
                                                                                  Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2003
25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR22137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                           hepatifis C virus nucleocapsid protein. The gene is positioned in a vector for efficient expression in prokaryotic cells. The expressed protein can be used in tests for the detection of antibodies specific for the HCV C protein. See also AAR74048. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "amino acid in this position is designated X in the specification, but codon usage shows that the only possible amino acid at this pos. is Gly"
                                          Vector for expression of a synthetically produced protein coding DNA - pref. encodes the hepatitis C virus nucleo-capsid protein which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
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                                                                                                                                                                       The sequence is that of a synthetic nucleotide sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus types 9a(7a) isolates FR1 amino acids 1-317,
                                                                                                                                                                                                                                                                                                                                                                   Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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د
                                                                                                                                                                                                                                                                                                                                                                   Score 977; DB 2;
Pred. No. 6.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Phe, Ser, Tyr, Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Ser, Pro, Thr, Ala
                                                                                       used in the detection of HCV antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                               Disclosure; Page 35; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR96546 standard; peptide; 319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Ile, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94EP-00870166.
                                                                                                                                                                                                                                                                                                                                                                   93.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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    N-PSDB; AAQ92070
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                                                                                                                                                                                                                                                                                                                           Sequence 196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                       Matches 176;
                                                                                                                                                                                                                                                                                   field.)
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RESULT 11 AAR96546

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Gaps

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Length 319;

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us-09-084-691b-206.rag

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180 180

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The sequence is that of NANB hepatitis virus HC-OM gene polypeptide P-733 -1. It may may be used in a system for detecting NANB hepatitis. This method is highly specific and sensitive, and can detect NANB hepatitis virus which could not be detected by conventional methods
  61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWGGWLLSPRGSRPSWGPTDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RRQPIPKVRRPEGRIWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen related to non-A and non-B hepatitis virus - comprises non-translation region comprising 340 - 341 mols. of nucleotides, non-translation region comprising 1885 - 2551 mols. of nucleotides including
                                          121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                                                                                                                                                                                                                                                                             Non-A, non-B; virus; polymerase chain reaction; detection; sensitive; specific; HCV; NANBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                    NANB hepatitis virus HC-OM gene polypeptide P-733-1.
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No. 2.8e-83;
9; J
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6; Mismatches
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                                                                                                                                                                       AAR38278 standard; protein; 733 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              91JP-00196175.
                                                                                                                                                                                                                                                                                                                                                                                                                                      90JP-00153401.
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92.1%;
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 92.1
les 176; Conservative
                                                                              181 LLSCLTTPASA 191
                                                                                                     LLSCLTVPASA 191
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                                                                                                                                                                                                                                                                                                                   Non-A.
non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1993-199637/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NAKA/) NAKAMURA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region 1,149 and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ43888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 733 AA;
                                                                                                                                                                                                                                                                                                                                                           JP05091884-A.
                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1990;
                                                                                                                                                                                                                          21-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                    6-APR-1993
                                                                                                                                                                                                AAR38278;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deoxyribonucleic acid sequence encoding non-A, non-B hepatitis virus -obtd. Hutch CS9 subgroup encoding polypeptide(s), useful as vaccines, and immuno reactive ABS for diagnosis of virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One Hutch strain (HCV-H) of NANBV, designated the Hutch c59 isolate (HCV-HC5) was propagated through passage in animals and the entire viral genome was cloned and sequenced (see AAQ22871). The sequence represented here comprises two amino acids, indicated in the features, which differ from the sequence of AAR2154. The proteins and peptides (see features) and antibodies against them are useful for the prepn. of vaccines and incoluums against NANBV and in immunological assays for detection of viral infection. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct
                                                                                                                                                                       "or Asn according to Seq No 46 (AAR22154), see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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Pred. No. 1.1e-83;
5; Mismatches 9; Indels
               1. .326
/label= NANBV_structural_proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prince AM;
                                                                                                                                                                                                                                                               /label= pref._envelope_antigen
                                                               1. .74
/label= pref._capsid_antigen
                                                                                         1. .20
/label= pref._capsid_antigen
                                                                                                                                                                              21...40
/label= pref._capsid_antigen
                                                                                                                                                                                                                          pref._capsid_antigen
                                                                                                                               'label= pref._capsid_antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 131-133; 225pp; English.
                                                                                                                                                                                                                                                 /label= envelope_protein
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ocation/Qualifiers
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                                      1. .120
/label= capsid
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91US-00748564.
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92.1%;
                                                                                                                                                        label= Ile
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                                                                                                                                                                                                           69. .120 /
/label= pr
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N-PSDB; AAQ22838.
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Best Local Similarity
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Gaps

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New synthetic peptides for detecting antibodies to hepatitis C virus -
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                                                                                          Hepatitis C virus; peptides; antibodies; ELISA.
                                AAR24440 standard, protein; 2894 AA.
                                                                             Composite HCV HC-J1/CDC/CHI protein.
                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pollet D, Maertens G,
                                                                                                                                                                                                                                                                                                                                                                                                                               90EP-00124241.
                                                                                                                                       7. .26
//abel= 2
//abel= 3
37 .56
//abel= 4
49. .68
//abel= 5
//abel= 6
//3. .92
//abel= 6
//3. .92
//abel= 6
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label= 10
712. .1731
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label= 14
263. .2282
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/label= 15
2275. .2294
/label= 16
2287. .2306
/label= 17
2299. .2318
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/label= 9
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/label= 11
1718. .1737
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|abel= 13
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label= 19
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/label= 1
                                                                 (first entry)
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181 LLSCLTVPASA 191
                                                          (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                   14-DEC-1990;
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                                                          25-MAR-2003
02-DEC-1992
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                                                                                                        Synthetic.
                                             AAR24440;
                                                                                                                                                                                                                                               Peptide
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Peptide
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RNA viruses frequently exhibit a high rate of spontaneous mutation, thus a virus is considered to be the same of equiv. to HCV if it exhibits a global homology of more than 70 percent with the HCV HC-VICCHI composite sequence. The peptide fragments of this DNA sequence indicated in the features table can immunologically mimic proteins encoded by HCV. Additional amino acids or chemical gps. may be added to either end of the peptides for the purpose of creating a linker arm for attachment to a carrier. The peptides can be used for the detection of antibodies specific for HCV. They may be used for the detection of antibodies specific for HCV. They may be used in the form of kits, opt. with reagents such as staphylococcal protein A, streptococcal protein G, avidin or streptavidin. The peptides may also be used as immunogens for raising antibodies. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
useful in e.g. ELISA assays, and for detection of HCV antigens or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 977; DB 2; Length 28
Pred. No. 1.3e-82;
6; Mismatches 9; Indels
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                                                                                                          Disclosure, Fig 1; 32pp; English
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92.1%;
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Best Local Similarity 92.1
Matches 176; Conservative
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181 LLSCLTVPASA 191
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07-NOV-1995
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                                              immunogens
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AAR70230 is the composite hepatitis C virus (HC-01/CDC/CHI) protein from which the synthetic HCV antigens described in AAR70210-R70229 were derived. These synthetic antigens can be used to screen blood, or blood products for the presence HCV, they can also be used in various specific assays for the detection of HCV antibodies, and antigens, or as immunogens. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.)
                                         Disclosure, Fig 1; 51pp; English.
and blood products.
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Sequence 2894 AA;

Gaps 0; Score 977; DB 2; Length 2894; Pred. No. 1.3e-82; 6; Mismatches 9; Indels (Query Match 93.5%; Best Local Similarity 92.1%; Matches 176; Conservative (

RROPI PKAROPOGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120 61

à 임 ð qq à Пр ŏ Пр

61 RRQPIPKVRRPBGRTWAQPGYPWPLYGNBGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120

KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

121

181 LLSCLTTPASA 191

[[[[]]]] LLSCLTVPASA 191 181 Search completed: October 30, 2004, 01:42:44 Job time : 157 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

October 30, 2004, 01:35:06 ; Search time 39 Seconds (without alignments) 471.215 Million cell updates/sec

US-09-084-691B-206 1045 1 MSTLDRKPQRKTKRNTNRRPT......CSFSIFLIALLSCLTTPASA 191

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			Cornertes	
Result No.	Score	Query	Query Match Length	DB	ID	Description
7	776	93.5	3011	-	S40770	genome polyprotein
71	916	93.4		Н	GNWVCH	
M	971	92.9		7	S12707	genome polyprotein
4	696	92.7	782	~	S18031	genome polyprotein
5	696	92.7	787	7	PN0677	hypothetical prote
9	968	92.6	3011	Н	GNWVC3	genome polyprotein
7	965	92.3	3010	٦	GNWVCJ	
8	965	92.3	3010	Н	GNWVTC	
6	962	92.1		7	JH0711	
10	961	92.0		7	JQ1584	
11	959	91.8		~	S32740	
12	958	91.7		7	S19876	genome polyprotein
13	957	91.6	513	7	PC1284	
14	957	91.6		~	S19875	genome polyprotein
15	957	91.6		N	PC2219	polypeptide - hepa
16	926	91.5		-1	GNWVTW	genome polyprotein
17	926	91.5	'n	Н	S18030	genome polyprotein
18	952	91.1		7	JQ1925	
19	951	91.0		~	PC2060	genome polyprotein
20	948	90.7	m	7	A45573	genome polyprotein
21	947	9.06	369	7	S21471	genome polyprotein
22	947	90.6		7	JQ1926	
23	947	90.6		7	S18032	genome polyprotein
24	946	90.5	4	7	S41288	
25	944	90.3	4	7	PC2061	genome polyprotein
26	941	90.0	874	N	JQ0883	genome polyprotein
27	940	90.0		ď	A44150	structural protein
28	939	89.9		7	JQ0881	genome polyprotein
29	939	89.9	3033	Н	JQ1303	

genome polyprotein	genome nolymptotein														
GNWVJB	PS0388	JN0265	JC5620	S41360	841361	PQ0393	S41346	841362	841363	841345	S41364	S41365	841366	541344	CA12EP
1 GNWVJB	2 PS0388	2 JN0265	1 JC5620	2 S41360	2 841361	2 PQ0393	2 S41346	2 841362	2 841363	2 841345	2 S41364	2 \$41365	2 \$41366	2 S41344	2 C413EB
-	2	7	יי	124 2 S41360	~	7 7	7	7	7	7	7	7	7	7	c
3033 1 (178 2 I	322 2	3014 1 0	7	123 2 8	266 2 E	118 2 5	114 2 8	117 2 8	115 2 8	115 2 8	114 2 8	114 2 8	115 2 8	2 6 411
89.6 3033 1 0	87.9 178 2 I	87.8 322 2	85.5 3014 1 0	124 2 8	60.8 123 2 8	60.4 266 2 E	59.9 118 2 8	59.0 114 2 8	58.6 117 2 8	58.5 115 2 8	58.4 115 2 8	58.3 114 2 8	57.9 114 2 8	57.9 115 2 8	2 6 111 9 53

ALIGNMENTS

genome polyprotein - hepatitis C virus N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) protein NS4, nonstructural protein NS4b; nonstructural protein NS5	protein M; hepacivirin (EC 3.4.21.98) (nonstructu 4b; nonstructural protein NS5
C;Species: hepatilis C virus C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change C;Accession: S40770; PC1285	19-May-2000 #text_change 09-Jul-2004
Kiukamoro, H. submitted to the EMBL Data Library, March 1992 A;Reference number: S40770	ch 1992
A,Accession: S40770 A,Molecule type: genomic RNA	
203463;	PIDN: BAA01582.1;
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Jpn. J. Exp. Med. 60, 167-177, 1990	Y.; YOLSUMOLO, S.; Tanaka, T.; YOShizawa, H.; TSUGA, The houstifis of mixed concess.
A; Itele: Inc. 3 - Celminal Sequence of the departies C vi.	ie meparitis C vilus gemonie. 16; PMID:2170712
 A; Accession: PC1285 A; Molecule type: quentic RNA	
 A; Cross-references: GB: D00831; NID: 9221511; PIDN: BAA00705.1;	511; PIDN:BAA00705.1; PID:9221512
A;Experimental source: isolate HC-J1 C:Superfamily: hepatitis C virus genome polyprotein	polyprotein
 C; Keywords: ATP; glycoprotein; hydrolase	C;Keywords: ATP; glycoprotein; hydrolase; nucleoting p-loop; polyprotein; serin
 F:115/Floudet: capsid process C #stack	us predicted kirks status predicted kEPM>
 F;192-389/Product: major envelope protein E #status predicted <mse> F;390-729/Product: nonstructural protein NS1 #status predicted <ns1< td=""><td>in E #status predicted <mee> n NS1 #status predicted <ns1></ns1></mee></td></ns1<></mse>	in E #status predicted <mee> n NS1 #status predicted <ns1></ns1></mee>
 F:1007-1615/Product: nonstructural protein NS2 #status pr F:1007-1615/Product: hepacivirin #status predicted <ns3></ns3>	protein NS2 #status predicted <ns2></ns2>
F:1230-1237/Region: nucleotide-binding motif A (P-loop)	motif A (P-loop)
F.1316-1319/Region: DEXH motif	COLL DEFINED SECOND SECONDS
F,1818-1862/Fibouct: Indistructural prote F,1863-2013/Product: nonstructural prote F,2014-3011/Product: nonstructural prote	
Query Match 93.5%; Score	Score 977; DB 1; Length 3011; Pred No 2 9e-74:
rative 6	Mismatches 9; Indels 0; Gaps 0;
 Qy 1 MSTLPKPQRKTKRNTNRRPTDVKFPC	MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
Db 1 MSTIPKPQRKTKRNTNRRPQDVKFP	MSTIPKPORKTKRNTNRRPQDVKFPGGGQIVGGVYLLFRRGPRLGVRATKKTSERSQPRG 60
 Oy 61 RROPIPKAROPOGRHWAOPGYPWPLY	RRQPIPKARQPQGRHWAQPGYPWPLYGNBGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
 DD 61 RROPIPKVRRPEGRIWAOPGYPWPL)	RRQPIPKVRRPEGRIWAQPGYPWPLYGNEGCGWAGWILSPRGSRPSWGPTDPRRESRNIG 120

121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180

à

o .

Gaps ·. 09

9

120

180

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C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C; Accession: S12707
R; Takeuchi, K.; Kubo, Y.; Boonmar, S.; Watanabe, Y.; Katayama, T.; Choo, Q.L.; Kuo, G.;
Nucleic Acids Res. 18, 4626, 1990
A; Title: Nucleotide sequence of core and envelope genes of the hepatitis C virus genome A; Reference number: S12707; MUID: 90356432; PMID: 2117749
A; Accession: S12707
A; Molecule type: genomic RNA
A; Residues: 1-441 < TAKS
                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q81776; EMBL:D00574; NID:g221656; PIDN:BAA00452.1; PID:g221
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Substitute polyprotein - hepatitis C virus (isolate JK2) (fragment)

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein

A;Variety: isolate JK2

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Boundited to the EMBL Data Library, September 1991

A;Reference number: S18029

A;Reference number: S18029

A;Reference number: S18039

A;Reference numbe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSTINPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRQPI PKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 441;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 971; DB 2; Length 44
Pred. No. 1.5e-74;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 92.9%;
Best Local Similarity 92.7%;
Matches 177; Conservative
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177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1683-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A36814
A;Molecule type: genomic RNA
A;Rosicues: 1-3011 <INC>
A;Cross-treferences: UNIPC>
A;Cross-treferences: UNIPCT: P27958; GB:M67463; NID:g329737; PIDN:AAA45534.1; PID:g329738
B;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A;Title: Genomic structure of the human prototype strain H of hepatitis C virus: compari
                                                                                                                                                                                                                                                                                                                                                                                                             (nonstructu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: A36814, A41546 - R. K. Inchestant, M.; Nasoff, M.; Prince, A.M. R. Inchauspe, G., Zebedele, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992 A;Description: Genomic structure of the human prototype strain H of hepatitis C virus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                       genome polyprotein - hepatitis C virus (strain H)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cypecies: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Reference number: A41546, MUID:92052256, PMID:1658800
A, Contents: annotation
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Best Local Similarity 92.7
Matches 177; Conservative
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                                                                                                                                                                                       181 LLSCLTVPASA 191
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                                                                                                                  LLSCLTTPASA
                                                                                                                  181
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A;Residues: 1577-1633 <CH2>
A;Residues: 1577-1633 <CH2>
A;Residues: 1577-1633 <CH2>
A;Residues: 2014-1633 <CH2>
A;Reperimental source: isolates E-b17
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstructural
C;Reywords: ATP; capsid protein C #status predicted <CPA>
F;116-191/Product: envelope protein M #status predicted <MEB>
F;192-389/Product: nonstructural protein NS1 #status predicted <NS1>
F;130-1006/Product: nonstructural protein NS1 #status predicted <NS2>
F;130-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;130-1137/Region: nucleotide-binding motif A (P-loop)
F;1316-1319/Region: DEXH motif
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R;Kato, N.; Hijkata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimot
R;Ritle: Molecular cloning of the human hepatitis C virus genome from Japanese patients
A;Recession: A39233
A;Molecule type: genomic RNA
A;Residues: 13010 (KAT)
A;Coss-references: UMPRROT: P26662; GB:D90208; NID: G221610; PIDN: BAA14233.1; PID: G221611
R;Kato, N.; Ohkoshi, S.; Shimotohno, K.
Proc. Jpn. Acad. 65B, 219-223, 1989
A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vari
A;Reference number: P80085
A;Reference number: P80086
A;Molecule type: genomic RNA
A;Residues: 2650-2707 (KA2)
A;Experimental source: Japanese isolate
C;Comment: The cleavage sites of this polyprotein have not been determined.
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; R-116,1941/P-ndure: envelone protein Mistaris michains of RPP.
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N.Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructura
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
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cal Similarity 91.6%;
175; Conservative 6
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
Drotein NS4a; nonstructural
Ecispecies: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A39166; P00403; P00404
R;Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coi
Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A;Title: Genetic organization and diversity of the hepatitis C virus.
A;Reference number: A39166; MUID:91172826; PMID:1848704
A;Residuss: 1-311 < CAD
A;Cross-references: UNIPROT:P26664; GB:M62321; NID:g328873; FIDN:AAA45676.1; PID:g329874
R;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L
J Gen. virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to e
A;Reference number: P00493; MUID:92268871; PMID:1316939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-787 <CHO.
A;Residues: 1-787 <CHO.
A;Residues: 1-787 <CHO.
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gen
                                                                                                                                                                                                                                                                                                                   hypothetical protein 787 - hepatitis C virus (fragment)
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 14-011-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
B;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
B;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
A;Title: Genomic typing of hepatitis C viruses from Korean patients: Implications of A;Reference number: PN0677; MUID:94059104; PMID:8240354
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Pred. No. 3.8e-74;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.7%;
Matches 177; Conservative
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A; Residues: 1577-1633 < CHA>
A; Cross-references: DDBJ:10128
A; Experimental source: isolates
                                                  191
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Genome polyprotein - hepatitis C virus (strain PRC1) (fragments)

N;Contains: envelope protein E1; envelope protein E2; nonstructural protein NS1; nonstructural structural protein NS1; nonstructural protein NS1; nonstructural protein NS1; nonstructural protein NS1; nonstructural protein NS2; pacession: JH0711

R;Liu, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchauspe, G.
Gene 114, 245-250, 1992

A;Title: Genomic typing of hepatitis C viruses present in China.

A;Reference number: JH0711; MUD: 92290283; PMID: 1318245

A;Reference number: JH0711; MUD: 92290283; PMID: 1318245

A;Residues: 1-550 cLIU>
A;Residu
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N;Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural prote C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1584
R;Kumar, U; Chang, D.; Thomas, H.; Monjardino, J.
J; Gan. Virol. 73, 1241-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative corrections of the structural region and expression of putative corrections of the structural region and expression of putative corrections of the structural region and expression of putative corrections of the structural protein of putative corrections of sequencing of the structural protein; PID:g64312C C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; nonstructural protein; polyprote; H;192-389/Product: core protein E1 #status predicted <EE>
F;192-389/Product: envelope protein E1 #status predicted <EE>
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Best Local Similarity 91.6%;
Matches 175; Conservative
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C'Superfamily: hepatitis C virus genome polyprotein

C'Superstands: AFP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura

F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <CPC>
F;192-389/Product: major envelope protein B #status predicted <NEB>
F;390-729/Product: major envelope protein MS1 #status predicted <NS2>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1230-1237/Region: mucleotide-binding motif A (P-loop)

F;1312-1317/Region: nucleotide-binding motif A (P-loop)
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R; Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.; Virol. 65, 1105-1113, 1991
A; Title: Structure and organization of the hepatitis C virus genome isolated from human A; Reference number: A38465; MUID:91140698; PMID:1847440
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A,Residues: 1-3010 <TAK>
A,Cross-references: UNIPROT:P26663; EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g3297
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                                                                                    F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010,209,234,250,305,325,411,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,
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protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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Fils1e-1319/Region: DEXH motif
Fils1e-1319/Region: DEXH motif
Fils1e-1319/Product: nonstructural protein NS4b #status predicted <N4b>
Fil86-2013/Product: nonstructural protein NS4 #status predicted <N4b>
Fil86-2013/Product: nonstructural protein NS5 #status predicted <NS5>
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Pred. No. 2.9e-73;
5; Mismatches 10; Indels
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Pred. No. 2.9e-73;
5; Mismatches 10; Indels
        nucleotide-binding motif
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92.1%;
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Best Local Similarity 92.1%;
Matches 176; Conservative
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Matches 176; Conserv
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                F;1312-1317/Region:
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R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus iso
A;Reference number: S18029
                                                                                          A.Accession: 819876
A.Molecule type: genomic RNA
A.Residues: 1-782 e4MO.
A.Cross-references: UNIPROT:068953; EMBL:X61595; NID:g59486; PIDN:CAA43792.1; PID:g59487
A.Experimental source: isolate JK5
C.Superfamily: hepatitis C virus genome polyprotein
C.Superfamily: hepatitis C virus genome polyprotein
C.Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;10-191/Product: core protein #status predicted <MAT1>
F;384-733/Product: No1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
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C;Species: hepatitis C virus
C;Species: J0-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1284
R;Accession: PC1284
Jpn. J. Exp. Med. 60, 167-177, 1990
A;Atitle: The S'-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712
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A,Residues: 1-513 <OKA>
A,Cross-references: UNIPROT:Q81221; GB:D00832; NID:g221513; PIDN:BAA00706.1; PID:g221514
C,Superfamily: hepatitis C virus genome polyprotein
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91.7%; Score 958; DB 2;
Best Local Similarity 91.6%; Pred. No. 3.2e-73;
Matches 175; Conservative 4; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 957; DB 2;
Pred. No. 2.6e-73;
5; Mismatches 11
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91.6%;
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Best Local Si
Matches 175;
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     F;390-640/Product: envelope protein E2 and nonstructural protein NS1 #status predicted < F;196,209,234,305,417,430,448,476,540,556,576,623/Binding site: carbohydrate (Asn) (cova
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N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2
C;Species: hepatitis C virus
A;Variety: isolate JKS
C;Date: 30-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyprotein - hepatitis C virus (isolate Russian) (fragment)
N;Contains: capsid protein C; envelope protein M
C;Species Hepatitis C virus
C;Decies Hepatitis C virus
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-20
C;Accession: S32740
R;Vassilev, V.B.; Viazov, S.O.; Kotova, E.Y.; Nosikov, V.V.
submitted to the EMBL Data Library, April 1993
A;Description: Evidence of new HCV variant of European isolate in Russia.
A;Reference number: S32740
A;Molecule type: genomic RNA
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                                                                        Length 640;
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6.9e-74;
                                                                                                                          11; Indels
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A;Cross-references: UNIPROT:Q68873; EMBL:X71407
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: capsid protein; envelope protein; polyprotein
C;Reywords: capsid protein C #status predicted <CPC>
F;1-115/Product: envelope protein M #status predicted <EPM>
                                                                        Score 961; DB 2;
Pred. No. 1.5e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 959; DB Pred. No. 6.9e-5; Mismatches
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Best Local Similarity 92.1%;
Matches 174; Conservative
                                                                      Query Match 92.0%;
Best Local Similarity 91.1%;
Matches 174; Conservative
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|LLSCLTVPASA 191
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                                                      genome polyprotein - hepatitis C virus (isolate JK3) (fragment)

N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
A;Variety: isolate JK3
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: 819875
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: Saquence analysis of putative structural regions of Hepatitis C Virus isc
A;Beference number: Saquence analysis of putative structural regions of Hepatitis C Virus isc
A;Reference number: 818029
A;Accession: 819875
A;A
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N. Contains: core protein; B1 (carboxyl end); B2/NS1 (amino end); NS3 protein; NS4A prote
C. Species: hepatitis C virus
C. Pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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A;Residues: 1-876 <STU>
A;Cross-references: UNIPROT:Q81242; GB:L29577; GB:L29579; GB:L29579
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Fil-19-17 Product: core #status predicted <COE>
Fil-19-17 Product: core #status predicted <COE>
Fig8-78 Region: variable relations with the status predicted <ERE>
Fil-19-2-247/Product: El (carboxyl end) #status predicted <ERE>
Fil-19-2-341/Product: El (samino end) #status predicted <ERE>
Fil-339-411/Region: NSI (amino end)
Fil-339-411/Region: NSI (amino end)
Fil-38-7-Froduct: NSI #status predicted <NSR>
Fil-38-7-Froduct: NSI #status predicted <NSR>
Fil-38-876/Product: NSI #status predicted <NSR>
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ilarity 91.6%; Pred. No. 3.9e-73;
Conservative 5; Mismatches 11;
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Best Local Similarity
Matches 175; Conserv
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F;281,287,294,312,340/Binding Bite: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                          1 MSTNPKPORKTKRNTNKRPODVKFPGGGOLVGGVYLLPRKGPRMGVRATRKTSERSOPKG 60
                                                                                                                                                    1 MSTLPKPORKTKRNTNRRPIDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                                                Score 957; DB 2;
Pred. No. 4.4e-73;
8; Mismatches 11;
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                                                91.6%;
nilarity 90.1%;
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                                                     Query Match
Best Local Similarity
Matches 172; Conserv
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Q81267 hepatitis c Q6x147 hepatitis c Aap6953 hepatitis c Q81274 hepatitis c Q81274 hepatitis c Q81274 hepatitis c Q81273 hepatitis c Q68157 hepatitis c Q68157 hepatitis c Q68157 hepatitis c Q68156 hepatitis c Q68116 hepatitis c Q68116 hepatitis c

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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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MEDLINE=92279243; PubMed=1317578;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the 5' noncoding region of hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
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Bukh J., Purcell R. H., Miller R. H.;

"At least 12 genotypes of hepatitis C virus predicted by sequence analysis of the putative E1 gene of isolates collected worldwide.";

Proc. Natl. Acad. Sci. U.S.A. 90.8234-8238 (1993).

EMBL. U10198; AAA21037.1; -.

GO; GO:0001902; C:viral capsid, IEA.

GO; GO:0001902; F:structural molecule activity; IEA.

InterPro; IPR00252; HCV capsid.

InterPro; IPR00251; HCV capsid.

Pfam; PF01543; HCV capsid.

Pfam; PF01542; HCV capsid. 1.
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BUBDILNES-84336721; PubMed=8058787;
Bukh J., Purcell R.H., Miller R.H.;
"Sequence analysis of the core gene of 14 hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1045; DB 2; Length 100.0%; Pred. No. 7e-80; ive 0; Mismatches 0; Indels
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 91:8239-8243(1994)
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NCBI_TaxID=11103;
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1045
1 MSTLPPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA
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- 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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BR GO; GO:0019028; C:viral capsid; IEA.

BR GO; GO:0019028; C:viral capsid; IEA.

BR GO; GO:0019021; C:viral envelope; IEA.

BR GO; GO:0019021; HCV capsid.

BR InterPro; IPR002521; HCV env.

BR InterPro; IPR002531; HCV env.

BR Ffam; PF01542; HCV core; 1.

BR Ffam; PF01542; HCV core; 1.

BR Ffam; PF01542; HCV N31; 1.

RR Ffam; PF01559; HCV N31; 1.

RR Ffam; PF01559; HCV N31; 1.

RR Ffam; PF01560; HCV N31; 1.

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                                                                            Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T., Ilzuka H., Mishiro S., Miyakawa Y., Mayumi M.; Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups."; Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
                                                                                                                                                                                                                                                                                                                                 Okamoto H.;
Snibmitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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Core, env and part of B2/NS1 (Fragment).
Virus.
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Pred. No. 7.3e-78;
1; Mismatches 3;
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MEDLINE=95062197; PubMed=7972001;
                                                          MEDLINE=95062197; PubMed=7972001;
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01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-JUN-2003 (TrEMBLrel. 24,
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PIR; PQ0804; PQ0804.
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Best Local Similarity
Matches 187; Conserv
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SEQUENCE FROM N.A.
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RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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Bernier L., Willems B., Delage G., Murphy D.G.;
"Identification of numerous hepatitis C virus genotypes in Montreal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Core protein (Fragment).
Hepatitis C virus type 6.
Hydruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepatitis C virus.
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBI_TaxID=11103;
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EMBL, U33435, AAB40038.1; -. GO: GO:0019028, C: Viral capsid; IEA.

GO: GO:005198; F: Structural molecule activity; IEA.
InterPro; IPR002522; HCV capsid.
InterPro; IPR02521; HCV core.
Pfam; PF01543; HCV core; 1.

NON_TER 191 191
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Pred. No. 4.8e-79;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         191 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 189; Conservative
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                                                                                                                              Matches 188; Conservative
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HSSP; P27958; IAIV.
                                                                                                                     Best Local Similarity
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                   1 MSTLPKPORKTKRNTNRRPTDVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG
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MEDLINE=95062197; PubMed=7972001;
TOkita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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                                                                                                                                                                                              Length 414;
                                                                                                                                                                                                                 3; Indels
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:iviral capaid; IEA.
GO; GO:001931; C:iviral envelope; IEA.
GO; GO:001931; C:viral envelope; IEA.
InterPro; IFR002522; HCV_capsid.
        Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                            414 AA; 44973 MW; F3F3CF154372F4FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                           Score 1024; DB 2;
Pred. No. 8.8e-78;
2; Mismatches 3;
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Hepatitis C virus.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Best Local Similarity 97.4%;
Matches 186; Conservative
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SEQUENCE FROM N.A.
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Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F., Miyakawa Y.,
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J. Gen. Virol. 79:1847-1857(1998).

EMBL; D84264; BAA32666.1; -.
InterPro; IPR002521; HCV_core.
InterPro; IPR002531; HCV_env.
InterPro; IPR002531; HCV_NS1.
Pfam; PP01543; HCV_cappid; 1.
Pfam; PP01542; HCV_core; 1.
Pfam; PP01559; HCV_env; 1.
Coar protein; Envelope protein; Glycoprotein; Nonstructural protein; NoN_TER 414 414
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R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:000526; F:ATP dependent helicase activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:000386; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:000526; F:serine-type peptidase activity; IEA.

R GO; GO:0005508; F:serine-type peptidase activity; IEA.

R GO; GO:0005508; F:serine-type peptidase activity; IEA.

R GO; GO:0005509; P:viral billocule activity; IEA.

R GO; GO:0019679; P:viral genome replication; IEA.

R GO; GO:0019679; P:viral transformation; IEA.

R GO; GO:0019679; P:viral transformation; IEA.
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Pred. No. 8.8e-78;
1; Mismatches 2;
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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                 R GO; GO:0016021, C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral binding; IEA.

R GO; GO:0008026; F:ATP binding; IEA.

R GO; GO:0008236; F:RNA directed RNA polymerase activity; IEA.

R GO; GO:0008236; F:serine-type peptidase activity; IEA.

R GO; GO:0008369; F:proteclysis and peptidolysis; IEA.

R GO; GO:0019079; F:viral genome replication; IEA.

R GO; GO:0019079; F:viral transformation; IEA.

R InterPro; IPR00345; CyCC heme BS.

R InterPro; IPR00345; CyCC heme BS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3018 AA; 329017 MW; 6E67FB3CF6A61AE3 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 8e-77;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      INCEPTO; IRRO02521; HCV capsid.
INCEPTO; IRRO02521; HCV capsid.
INCEPTO; IRRO02511; HCV core.
INCEPTO; IRRO02511; HCV core.
INCEPTO; IRRO02511; HCV N34.
INCEPTO; IRRO0745; HCV N34b.
INCEPTO; IRRO01490; HCV N34b.
INCEPTO; IRRO04190; HCV N34b.
INCEPTO; IRRO04109; Peptidase S29.
INCEPTO; IRRO04109; Peptidase S29.
INCEPTO; IRRO02618; Pept U39 HCV N32.
INCEPTO; IRRO07095; RNA_POI_DS_PF.
INCEPTO; IRRO07095; RNA_POI_DS_PF.
PEam; PF01543; HCV capsid; I.
PEam; PF01543; HCV capsid; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF01538; HCV_NS2; 1.
Pfam, PF02907; HCV_NS3; 1.
Pfam, PF01006; HCV_NS4s; 1.
Pfam, PF01001; HCV_NS4b; 1.
Pfam, PF01506; HCV_NS5a; 1.
Pfam, PF00998; Viral_RdRP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 97.9
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00487; DEXDC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLSCLTTPASA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01560; HCV_NS1;
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Best Local S
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HHAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRQPIPKARQSQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPNWGPNDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyprotein.
Hepatitis C virus type 6a.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Hepatitis C virus type 6.
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MEDLINE=97320431; PubMed=9177282;
MAdams A., Chamberlain R.W., Taylor L.A., Davidson F., Lin C.K., Simmonds P., Elliot R.M.;
"Complete coding sequence of hepatitis C virus genotype 6a.";
Blochem Biophys. Res. Commun. 234:393-396(1997).
HSSP; P27958; IAIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3016 AA; 328032 MW; 4E5CFF96258BCE3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3018 AA.
                                                                                                InterPro; IPR00145; HCV_NS41.
InterPro; IPR001490; HCV_NS42.
InterPro; IPR001490; HCV_NS43.
InterPro; IPR00166; HCV_NS45.
InterPro; IPR002166; HCV_RGRP.
InterPro; IPR004109; Peptidase_S29.
InterPro; IPR004003; Pept_U39_HCV_NS2.
InterPro; IPR007031; Pept_U39_HCV_NS2.
InterPro; IPR007094; RNA_pol_DS_PS.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01500; HCV_NS3; 1.
Pfam; PF01006; HCV_NS3; 1.
Pfam; PF01006; HCV_NS42; 1.
Pfam; PF01006; HCV_NS42; 1.
HCV_capsid
HCV_core.
                                                    IPR002519; HCV_env.
IPR002531; HCV_NS1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00487; DEXDC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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  FR002522;
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Matches 188; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                          InterPro;
InterPro;
                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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61 RRÓPIPKARQPIGRHWAQPGYAWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KVIDTITCGFADLMGYIPVLGAPLGGVAAALAHGVRVIEDGINYATGNLPGCSFSIFLLA 180
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                                                                                                                                                                                                                                                                                                                                                                                                               UnterPro; IPR00252; HCV capsid.
InterPro; IPR00252; HCV capsid.
InterPro; IPR002521; HCV capsid.
InterPro; IPR002519; HCV capsid.
InterPro; IPR002519; HCV cap.
InterPro; IPR002519; HCV cap.
InterPro; IPR002519; HCV capsid; 1.
Pfam; PP01549; HCV core; 1.
Pfam; PP01549; HCV core; 1.
Pfam; PP01559; HCV cap. 1.
Pfam; PP01550; HCV cap. 1.
Pfam; PP01560; HCV cap. 1.
Polyprotein; InterPro; IPR0050; HOV cap. 1.
Polyprotein; Iransmembrane.
NON_TER 414 414
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   Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T., Ilzuka H., Mishiro S., Miyakawa Y., Mayumi M.; Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.", Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1016; DB 2; Length 414;
Pred. No. 4.1e-77;
2; Mismatches 4; Indels
                                                                                                                                                                                                                    Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
BMBL; D88470; BAA13619.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D88473; BAA13622.1; -.
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| SEQUENCE FROM N.A.
| MEDLINE=95062197; PubMed=7972001;
| MEDLINE=95062197; PubMed=7972001;
| MEDLINE=97062197; PubMed= 8.,
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01-MAY-1997 (TrEMBLrel. 03, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44850 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.9
Matches 185; Conservative
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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Polyprotein; Transmembrane.
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                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=95062197; PubMed=7972001;
Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cokamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL;
COMPOSED (C. integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR009100; AcylCoA_dehyd_NM.
InterPro; IPR002521; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002521; HCV_core.
R InterPro; IPR002531; HCV_core.
R InterPro; IPR01543; HCV_core.
R InterPro; IPR01542; HCV_core.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Core, env and part of E2/NS1 (Fragment). Hepatitis C virus.
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Hepatitis C virus.
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Pfam; PF01542; HCV core; 1.
Pfam; PF01539; HCV env; 1.
Pfam; PF01560; HCV N31; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON TER 414 414
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Hepacivirus.
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Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K., Chainuvati T., Iizuka H., Teuda F., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Thailand classifiable into i genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1011; DB 2; Length 414; Pred. No. 1.1e-76; 0; Mismatches 5; Indels
                                                                                                                                                                                                Length 414;
                                                                                                                                                                                                                                             3; Indels
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J. Gen. Virol. 76.2329-2335(1995).

S. Gen. Virol. 76.2329-2335(1995).

R GO; GO: 001021; C: integral to membrane; IEA.

GO; GO: 001021; C: integral to membrane; IEA.

GO; GO: 00103021; C: viral capsid; IEA.

GO; GO: 0019021; C: viral envelope; IEA.

GO; GO: 00190218; F: structural molecule activity; IEA.

InterPro; IPR00252; HCV_core.

InterPro; IPR002521; HCV_core.

InterPro; IPR002519; HCV_core.

InterPro; IPR002531; HCV_core.

R Fam; PP01543; HCV_core.
                                                                                                                                                 695600C405A2C082 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Core, env and part of E2/NS1 (Fragment).
Hepatitis C virus.
                                                                                                                                                                                              97.0%; Score 1014; DB 2; 96.9%; Pred. No. 6.1e-77; ive 3; Mismatches 3;
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                                                                                                                                              SEQUENCE 414 AA; 44892 MW;
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NON TER 414 414
SEQUENCE 414 AA; 44994 M
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Best Local Similarity 97.4
Matches 186; Conservative
                                                                                                                                                                                                                                             Matches 185; Conservative
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                                                                                                                                                                                                                       Similarity
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                    R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0019028; C:viral capsid; IEA.
R GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019018; C:viral envelope; IEA.
GO; GO:0019018; F:structural envelope; IEA.
R InterPro; IPR002522; HCV capsid.
R InterPro; IPR002521; HCV core.
R InterPro; IPR002531; HCV core.
R InterPro; IPR002531; HCV SI.
R Pfam; PR01543; HCV capsid; 1.
R Pfam; PR01543; HCV capsid; 1.
R Pfam; PR01543; HCV corr; 1.
R Pfam; PR01560; HCV NS1; 1.
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Hepacivirus.
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D88472; BAA13621.1; -.
EMBL; D88472; BAA13621.1; -.
EMBL; D804029; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019031; C:viral capsid; IEA.
R GO; GO:005198; F:structural molecule activity; IEA.
R InterPro; IPR00522; HCV capsid.
R InterPro; IPR002519; HCV env.
R Pfam; PF01543; HCV_capsid.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 1016; DB 2; 96.9%; Pred. No. 4.1e-77; ative 1; Mismatches 5
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MEDLINE=95062197; PubMed=7972001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 185; Conservative
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RESULT 11 P89959

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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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DR GO; GO: 0016021; C: or nee EmbL/Genbank/DDBJ databases.
BC GO; GO: 0016021; C: or nee Embrane; IEA.
DR GO; GO: 0019028; C: or nee Embrane; IEA.
DR GO; GO: 0019028; C: or nee Embrane; IEA.
DR GO; GO: 0019028; C: or nee Embrane; IEA.
DR GO; GO: 0019028; C: or nee Embrane; IEA.
DR GO; GO: 0019028; C: or nee Embrane; IEA.
DR GO; GO: 0019028; F: structural molecule activity; IEA.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002521; HCV core.
DR InterPro; IPR002521; HCV core.
DR Ffam; PP01543; HCV core; 1.
DR Pfam; PP01544; HCV core; 1.
DR Pfam; PP015
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Hepacivirus.
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Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Tizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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Hepatitis C virus.
                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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         181 LLSCLTTPASA 191
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01-NOV-1998 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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and molecular analysis of untypeable samples.";
Wirus Res. 38:137-157(1995).
BMBL; L38339; AA0421931.;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019038; C:viral envelope; IEA.
GO; GO:001998; F:structural molecule activity; IEA.
InterPro; IPR002521; HCV.core.
InterPro; IPR002519; HCV.core.
InterPro; IPR002519; HCV.core.
InterPro; IPR002519; HCV.core.
INR Pfam; PP01543; HCV.core; I.
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                                                                                                                                   RROPIPKARHOTGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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Stuyver L., Wyseur A., van Arnhem W., Lunel F., Laurent-Puig P., Pawlotsky J.-M., Kleter B., Bassit L., Nkengasong J., van Doorn L.-J., Maertens G.;
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Hepacivirus; Hepatitis C virus type 6.
NCBI_TaxID=31655;
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MEDLINE=96118171; Pubmed=8578855;
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Hepatitis C virus type 6a.
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AC Q68703
DT Q68703
DT O1-NOV-
DT O1-JUN-
DE CORE PR
OS HEPACIV
OX NCBL TA
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                         MEDLINE=97060095; PubMed=8904416;

MEDLINE=97060095; PubMed=8904416;

A Doi H., Aphichartpiyakul C., Ohba K., Mizokami M., Hotta H.;

A Doi H., Aphichartpiyakul C., Ohba K., Mizokami M., Hotta H.;

Thepatitis C virus (HVV) subtype prevalence in Chiang Mai, Thailand, and identification of novel subtypes of HCV major types 6.";

I. Clin. Microbiol. 34:569-574(1996).

B EMBL; D63946; BAA09976.1;

CO:0019028; C:viral capsid, IEA.

R GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR002522; HCV_capsid.

R InterPro; IPR002521; HCV_capsid.

R Pfam; PF01543; HCV_core:

R Pfam; PF01142; HCV_core:

R Pfam; PF01144; HCV_core:

R Pfam
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Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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191 191
191 AA, 20727 MW, 411C1C851ADA2DB5 CRC64,
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96.4%; Score 1007; DB 2;
Best Local Similarity 95.3%; Pred. No. 1.1e-76;
Matches 182; Conservative 5; Mismatches 4;
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-290-665A-193
PCT-US95-10398-193
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PCT-US95-10398-194
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US-08-35-886C-217
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APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: AND ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
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15-AUG-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 UINE 1993
PRIOR APPLICATION NUMBER: 08/290/665
PILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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TELEFAX: (212) 751-6849
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APPLICATION NUMBER: PCT
FILING DATE: 15-AUG-199
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INFORMATION FOR SEQ ID NO:
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Query Match

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APPLICANT: DELEYS, Robert
APPLICANT: BELEYS, Robert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
TITLE OF INVENTION: VIRUS
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2752-18
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT APPLICATION NUMBER: D96-04-25
PRIOR PELING DATE: 1996-04-25
PRIOR PELING DATE: 1994-10-28
PRIOR PLING DATE: 1993-11-04
NUMBER OF SEC ID NOS: 286
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 228
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                                                                                                                        1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                         Indels
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100.0%; Pred. No. 1.7e-96;
iive 0; Mismatches 0;
al Similarity 100.0%; Pred. No. 9.3e-97; 191; Conservative 0; Mismatches 0;
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Patent No. 661333
GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
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APPLICANT: LEROUX-ROELS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-228
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Best Local Similarity 100.
Matches 191; Conservative
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UMBER: PCT/US95/10398
15-AUG-1995
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REFERENCE/DOCKET NUMBER: 2026-4116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/290/665
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                                                      191:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION NUMBER: PCT/US
(212) 758-4800
(212) 751-6849
                                                                                                                                                                                                                                                              95.3%;
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FILING DATE: 15 AUGUST 1:
ATTORNEY/AGENT INFORMATION:
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                                   TELEX: 421792
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
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NEW YORK
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TITLE OF INVENTION: AMIN
TITLE OF INVENTION: AND
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQUENCES: 2620 NUMBER OF SEQUENCES: 263
                                                                                                                                                                                       ORGANISM: homosapiens
;
INDIVIDUAL ISOLATE: Z4
US-08-290-665A-191
                                                                                                                                                                                                                                                                Query Match 95.3
Best Local Similarity 94.8
Matches 181; Conservative
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                                                                                                                               unknown
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MEDIUM TYPE: FLOPPY COMPUTER: IBM PC COM
                                                                                                                                                unknown
                                                                                                               TYPE: amino acid
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                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                               STRANDEDNESS:
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 TELEPHONE:
TELEFAX: (
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             TITLE OF INVENTION: UNEUG
TITLE OF INVENTION: UNEUG
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT FILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATENTIN NUMBER: POSTIB:6
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
NUD THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 191, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKK, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
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       MAERIENS, Geert
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NEW YORK
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                                                                                                                                                                                                                                  SEQ ID NO 228
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STATE:
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                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                    LENGTH:
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61 RRQPIPKARQPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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                                                                                                                                                                                              61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                           1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                         1 MSINPKPQRKIKRNINRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                     Gaps
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                    0
Length 191;
                                                    6; Indels
    Score 996; DB 2;
Pred. No. 7.3e-92;
4; Mismatches 6
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61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                        Length 191;
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                                                                                                                                                                                                                                                    Score 982; DB 2;
Pred. No. 1.8e-90;
5; Mismatches 7
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APPLICATION NUMBER: US/08/290,665A FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
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NAME: RICHARD W BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-290-665A-193
; Sequence 193, Application US/08290665A
; Patent No. 5882852
; GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS: ADDRESSE: MORGAN & FINNEGAN
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                      94.0%;
93.7%;
                                            LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
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INFORMATION FOR SEQ 1D NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
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                                                                                                                                                             ORGANISM: homosapiens INDIVIDUAL ISOLATE: 28
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Best Local Similarity 93.7
Matches 179; Conservative
  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RRQPIPKARQPEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 192, Application US/08290665A

Patent No. 588285.

GENERAL INFORMATION:

APPLICANT: BURH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.

TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: COR GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THEISE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THEISE
TITLE OF INVENTION: ASCOURAGES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                           Length 191;
                                                                                                                                                                                                                                                                                                                                    95.3%; Score 996; DB 5; 94.8%; Pred. No. 7.3e-92; iive 4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION WIMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/290,665A FILING DATE: 15-AUG-1994 CLASSIFICATION: 435
                TELEPHONE: (212) 758-4800
TELERA: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: FLOPPY DISK
IBM PC COMPATIBLE
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TELEFAX: (212) 751-6849
TELEX: 421792
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NAME: RICHARD W. BORK
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LLSCLTTPASA 191
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181 LLSCLTVPASA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 181; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEW YORK
                                                                                                                                                                                                  TOPOLOGY: unk
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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STREET: 34
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TITLE OF INVENTION: NUCLECTIDE AN TITLE OF INVENTION: AMINO ACID SE TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: AMINO ACID SE TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     Query Match
Best Local Similarity 93.77
Matches 179; Conservative
                                                  ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: Z8
                  SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 LLSCLTTPASA 191
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TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10154
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                                                                                                            PCT-US95-10398-192
                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                      KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                                                                                                                                                                                                               1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                             Gaps
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ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                           .;
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                                                                                                                                   Score 982; DB 2; Length 191;
Pred. No. 1.8e-90;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLECTIBE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: PCT/US95/10398
15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NUMBER: PCT/US95/10396
FILING DATE: 125 AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-10398-192; Sequence 192, Application PC/TUS9510398; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                       94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: RICHARD W. BORK
                                                                                                                                                                             Matches 179; Conservative
                        TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
INDIVIDUAL ISOLATE: Z1
      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSCLTTPASA 191
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NEW YORK
                                                                                                                                       Query Match
Best Local Similarity
      STRANDEDNESS:
                                                                                                  US-08-290-665A-193
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61 RRQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRKSRNLG 120
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                                                                                                                                          1 MSTADRKPORKTKRATANRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                   1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                      121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
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NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                       .
  Length 191;
94.0%; Score 982; DB 5;
93.7%; Pred. No. 1.8e-90;
iive 5; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 193, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
COMPATER: IBM PC-DOS/MS-DOS
SOFTWARE: WORDPERPECT 5.1
CURRENT APPLICATION DATA:
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Gaps

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KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
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                                                                                                                                                                                                                            1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGCVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                             1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                          61 RRQPIPKARQPBGRIWAQPGYPWPLYGNEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE SERIES OF PREPAITIES C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                              Length 191;
                                                                                                       93.9%; Score 981; DB 2; Length 19
93.7%; Pred. No. 2.3e-90;
ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/10398 FILING DATE: 15-AUG-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 172, Application PC/TUS9510398 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MUCLEOTIDE A TITLE OF INVENTION: AMINO ACID SITILE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REPERINCE/DOCKET NUMBER: 2026
TELECOMUTUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: FLOPPY DISK COMPUTER: IBM PC COMPUTELE SOPERATING SYSTEM; PC-noc/wo
                        RGANISM: homosapiens
NDIVIDUAL ISOLATE: HK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 191 amino acids TYPE: amino acid
                                                                                                                                               Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK STATE: NEW YORK
  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS:
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US-08-290-665A-172
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                          ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KVIDTLTCGFADLMGYIPVVCAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RROPIPKAROPOGRHWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                     1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSBRSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                           Length 191;
                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                         Score 982; DB 5;
Pred. No. 1.8e-90;
                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: 0.5A

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: 1BM FC CONTAILBLE
COMPUTER: 1BM FC CONTAILBLE
COMPUTER: 1BM FC CONTAILBLE
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 15-AUG-1994
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-290-665A-172; Sequence 172, Application US/08290665A; Parent No. 5882852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 421792
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     Query Match
Best Local Similarity 93.7%;
Matches 179; Conservative
191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORGAN & FIN STREET: 345 PARK AVENUE
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                                                                               ....canISM: homosapiens
;
PCT-US95-10398-193
                                       unknown
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                 TYPE: amino acid
STRANDEDNESS: unkn
TOPOLOGY: unknown
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RY: USA
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Best Local Similarity
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STRANDEDNESS:
TOPOLOGY: unkr
                                                                             ORIGINAL SOURCE:
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                   121 KVIDTLITCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                        1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                     1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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NUCLECTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORR GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                      Length 191;
                                      93.8%; Score 980; DB 2; 93.7%; Pred. No. 2.9e-90;
                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10396
FILING DATE: 15-AUG-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 197, Application PC/TUS9510398 GENERAL INFORMATION:
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APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
FILING DATE: 15 AUGUST 1994
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AN
TITLE OF INVENTION: AMINO ACID SE
TITLE OF INVENTION: CORE GENES OF
TITLE OF INVENTION: SEQUENCES IN
TITLE OF INVENTION: SEQUENCES IN
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 205
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
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CITY: NEW YORK
STATE: NEW YORK
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                                                         Best Local Similarity 93.7
Matches 179; Conservative
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STRANDEDNESS: unknown
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ORIGINAL SOURCE:
ORGANISM: homosapi
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US-08-290-665A-197
                                        Query Match
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                                                                                                                                                                Gaps
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                                                                                                                     Score 981; DB 5; Length 191;
Pred. No. 2.3e-90;
5; Mismatches 7; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
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NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 197, Application US/08290665A; Patent No. 5882852
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INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
                                                                                                                       93.98;
93.78;
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INDIVIDUAL ISOLATE: DK13
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TYPE: amino acid
                   INDIVIDUAL ISOLATE: HK3 PCT-US95-10398-172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCL.
TITLE OF INVENTION: AMINITITLE OF INVENTION: AND TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 263 CORRESPONDENCE ADDRESS:
                                                                                                                                                                Matches 179; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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TOPOLOGY: unknown
    TOPOLOGY: unknown
                                                                                                                     Query Match
Best Local Similarity
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NEW YORK
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Batent No. 6555114

GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: URUS
FILE REFERRANCE: 2752-18

CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT APPLICATION NUMBER: US/08/635,886C
CURRENT APPLICATION NUMBER: BP6-04-25
PRIOR APPLICATION NUMBER: BP6-04-25
PRIOR PILING DATE: 1994-10-23
PRIOR APPLICATION NUMBER: BP 3402718.6
PRIOR FILING DATE: 1994-10-4
NUMBER OF SEQ ID NOS: 286

SOFTWARE: Patentin version 3.1
SEQ ID NO 2.17
                                                                                                                                                                                                                         61 RRQPIPKARQLEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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                                                        Length 191;
                                                                                          8; Indels
                                                    Score 980; DB 5;
Pred. No. 2.9e-90;
4; Mismatches 8;
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                                                    Query Match 93.8%;
Best Local Similarity 93.7%;
Matches 179; Conservative
INDIVIDUAL ISOLATE: DK13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: hepatitis C virus
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Matches 179; Conservative
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     PCT-US95-10398-197
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US-08-635-886C-217
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| Canz 6/ptodata/1/pubpaa/US07 PUBCOMB.ppp:*

| cgn2 6/ptodata/1/pubpaa/US06 PUBF PUB.ppp:*

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| cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.ppp:*

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| cgn2 6/ptodata/1/pubpaa/US106 PUBCOMB.ppp:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                    OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                           Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		æ				
Result		Query				-
No.	Score	Match	Match Length DB	DB	QI	Description
	1045	100.0	319	15	US-10-651-165-228	Sequence 228, App
7	980	93.8	319	15	US-10-651-165-217	Sequence 217, App
٣	977	93.5	319	σ	US-09-851-138-42	Sequence 42, Appl
4	977	93.5	319	15	. US-10-651-165-229	Sequence 229, App
5	977	93.5	450	15	US-10-651-165-181	Sequence 181, App
9	977	93.5	2894	6	US-09-941-611-23	Sequence 23, Appl
7	977	93.5	2894	14	US-10-044-995-23	Sequence 23, Appl
80	916	93.4	249	15	US-10-365-620-54	Sequence 54, Appl
σ	916	93.4	450	15	US-10-651-165-179	Sequence 179, App
10	916	93.4	450	15	US-10-651-165-180	Sequence 180, App
11	916	93.4	473	15	US-10-365-620-56	Sequence 56, Appl
12	916	93.4	3011	6	US-09-742-659-4	Sequence 4, Appli
13	976	93.4	3011	σ	US-09-952-572-9	Sequence 9, Appli

200000000000000000000000000000000000000	Sequence 1, Appli Sequence 48, Appl Sequence 231, Appl Sequence 7, Appli Sequence 50, Appli Sequence 50, Appli Sequence 50, Appl
US-09-929-955-1 US-09-747-419-2 US-09-891-894-1 US-10-184-150-1 US-10-184-150-1 US-10-184-150-1 US-10-184-150-1 US-10-184-150-1 US-10-184-150-1 US-10-184-150-1 US-10-195-734-1 US-09-995-937-1 US-09-995-937-1 US-09-995-937-1 US-09-995-937-1 US-09-995-937-1 US-09-995-937-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1 US-10-651-165-1	4 US-10-268-562-1 US-09-851-138-48 5 US-10-651-165-231 5 US-10-450-649-7 US-09-973-025-50 0 US-09-899-303-50 0 US-09-995-808-50
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ALIGNMENTS

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y sequence 228, Application US/10651165
y Bublication No. US20040047877A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEREOUX-ROBLS, Geart
APPLICANT: DELEXYS, Robert
TITLE OF INVENTION: URMUNOCMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-110-28
PRIOR FILING DATE: 1997-110-28
PRIOR FILING DATE: 1993-110-4
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
FEQUENCE: PATENTIN OF SEQ ID NOS: 286
SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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Best Local Similarity 100.0%; Pred. No. 1.1e-83;
Matches 191; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: hepatitis C virus US-10-651-165-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120

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61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KVIDTLTXXLADLMGYIPVLGGPLGGVAAALAHGVRAIEDGVNYATGNLPGCSFSIFLLA 180
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APPLICANT: DELEYS, ROBERT
APPLICANT: MARRIENS, Geert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REFRENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR APPLICANION NUMBER: DET/EP94/03555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RRQPIPKVRQPTGRSWGQPGYPWPLYGNBGCGWAGWLSPRGSRPNWGPNDPRRRSRNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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0
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                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
FILING DATE: 05-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 977; DB 9; L. Pred. No. 1.1e-77; 3; Mismatches 9;
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/836,075
FILING DATE: «UDKNOWN)
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 OCT 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 JUN 1995
ATTORNAY AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REGISTRANCE/DOCKET NUMBER: 29,775
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1994-10-28
APPLICATION NUMBER: EP 93402718.6
FILING DATE: 1993-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 229, Application US/10651165
Publication No. US2004004787131
BERERAL INFORMATION:
APPLICANT: LEROUX-ROBLS, Geert
                                                              COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.5%;
93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity 93.7
Matches 179; Conservative
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181 LLSCLTTPASA 191
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NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RRQPIPKARQLEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EDITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EDITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REPERBENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT FILING DATE: 1997-11-19
FRIOR FILING DATE: 1997-11-19
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1993-11-04
FRIOR FILING DATE: 1993-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSTLPKPORKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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Pred. No. 5.9e-78;
4; Mismatches 8;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                  Sequence 217, Application US/10651165
Publication No. US20040047877A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42, Application US/09851138 Publication No. US20020183508A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MAERTENS, GEERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENTS
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Best Local Similarity 93.7%;
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEROUX-ROELS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: hepatitis C virus US-10-651-165-217
                                                                                                                                              LLSCLTTPASA 191
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|LSCLTVPASA 191
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TITLE OF INVENTION:
                                                                                                                                                                                                                                             RESULT 2
US-10-651-165-217
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US-09-851-138-42
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61 RROPIDKVRRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLG 120
                                                                                                                                                                                     1 MSTIPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                              KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTIGENS FOR THE DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 977; DB 9; Length 2894; Pred. No. 1.2e-76; 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/941,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAERTENS, GEERT
VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETEC
ANTIBODIES TO HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-Aug-2001
CLIASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/391,671
FILING DATE: 1995-60-21
FILING DATE: 1955-62-21
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: EP 90124241.2
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1487-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-941-611-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 7038164000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09941611 Patent No. US20020106640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DELEYS, ROBERT J
POLLET, DIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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92.1%;
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                        LLSCLTTPASA 191
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Publication No. US20040047877A1

GENERAL INFORMATION:

APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

APPLICANT: DELEYS, Robert

TITLE OF INVENTION: URNUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: UNDOMINER: US/08/974,690C

PRIOR PELICATION NUMBER: DET/EP94/03555

PRIOR PELICATION NUMBER: PCT/EP94/03555

PRIOR APPLICATION NUMBER: PCT/EP94/03555

PRIOR PILING DATE: 1994-10-28

PRIOR PILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: PLEAFILIN VETSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 977; DB 15;
Pred. No. 1.1e-77;
3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 977; DB 15;
Pred. No. 1.6e-77;
6; Mismatches 9;
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; OTHER INFORMATION: Xaa is any amino acid
US-10-651-165-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.5%;
92.1%;
                                                                                                                                                                                                                                                                                LOCATION: (308)..(308)
OTHER INFORMATION: Xaa is any
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.5%;
Best Local Similarity 93.7%;
                                     PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: hepatitis C virus
                                                                                                                 ORGANISM: hepatitis C virus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similation
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 176; Conservative
                                                                                                                                                                                       LOCATION: (128)..(129)
OTHER INFORMATION: Xaa is
FEATURE:
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|LLSCLTTPASA 191
                NUMBER OF SEQ ID NOS: 286
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE LOCATION: (310)..(310)
                                                                                                                                                                                                                                                             NAME/KEY: MISC FEATURE
                                                                                                                                                                       NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                  SOFTWARE: Pate
SEQ ID NO 229
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Par
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                                                                                                        TYPE: PRT
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Query Match Best Local Similarity 92.1 Matches 176; Conservative 1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60

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APPLICANT: George, Rajan
APPLICANT: Tyrrell, Lorne
APPLICANT: Tyrrell, Lorne
APPLICANT: Tyrrell, Lorne
TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
FILE REFERENCE: 656.001
CURRENT APPLICATION NUMBER: US/10/365,620
CURRENT FILING DATE: 2003-02-13
PRIOR PLING DATE: 2003-11-05
PRIOR PLING DATE: 2003-11-05
PRIOR PLING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.2
SQTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                           121 KVIDTLICGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA
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                                                Gaps
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Length 2894;
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                                             Indels
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93.5%; Score 977; DB 14; 92.1%; Pred. No. 1.2e-76; iive 6; Mismatches 9;
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5; Mismatches
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GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 54, Application US/10365620
; Publication No. US20040001853A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) TYPE: PRT
; ORGANISM: ORF of HCV Core Protein
US-10-365-620-54
Query Match
Best Local Similarity 92.1:
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.4
Best Local Similarity 92.7
Matches 177; Conservative
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                                                                                    RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                                                                                         KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                             9
                         1 MSTIPKPQRKTKRNTNRRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                  MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAERTENS, GEERT
VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
ANTIBODIES TO HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/391,671
FILING DATE: -Unknown>
FILING DATE: -UNKnown>
FILING DATE: 14-0CT-1992
APPLICATION NUMBER: WO PCT/EP91/02409
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: EP 90124241.2
FILING DATE: 14-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,995
FILING DATE: 15-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 146
TELECOMUNICATION INFORMATION:
TELEPHONE: 7038164000
                                                                                                                                                                                                                                                                                                                                                                         RESULT ,
US-10-044-995-23
US-10-044-995-23
; Sequence 23, Application US/10044995
; Publication No. US20030049685A1
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT J
; POLLET, DIRK
POLLET, DIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                      181 LLŚCLTVPAŚA 191
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; TYPE: PRT
; ORGANISM: ORF of HCV Core-TBD protein
US-10-365-620-56
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Ingravallo, Paul
Wright-Minogue, Jacquelyn
Lau, Johnson Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09742659; Patent No. US20010034019A1; GENERAL INFORMATION:
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Butkiewicz, Nancy J.
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; Sequence 180, Application US/204047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEVEX, Robert
; TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; FRICK APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR FILING DATE: 1997-11-028
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NUMBER: EP 93402718.6
; SOFTWARE: PALENTIN VAMBER: EP 93402718.6
; SOFTWARE: PALENTIN VATES OF 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PALENTIN VATES OF 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PALENTIN VATES OF 1993-11-04
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; SOFTWARE: PALENTIN VATES OF 1993-11-04
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; SOFTWARE: PALENTIN VATES OF 1993-11-04
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; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PALENTIN VATES OF 1993-11-04
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APPLICANT: DELEIN NOZE:
APPLICANT: MAERTENS, GGERT
TITLE OF INVENTION: INMUNOOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: URBOR
TITLE OF INVENTION: URBOR: US/10/651,165
CURRENT APPLICATION NUMBER: US/00/03
PRIOR RAPLICATION NUMBER: US/00/03
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR PILING DATE: 1997-11-0-28
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR PILING DATE: 1993-11-0-4
PRIOR FILING DATE: 1993-11-0-4
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Pred. No. 1.9e-77;
5; Mismatches 9;
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Best Local Similarity 92.7%;
Matches 177; Conservative
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Best Local Similarity
Matches 177; Conserv
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US-10-651-165-180
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                                                                                                                                                                                 WENDLY ABOUT 10-365-620-56

Sequence 56, Application US/10365620

Publication No. US20040001853A1

GENERAL INFORMATION:

APPLICANT: George, Rajan

APPLICANT: Tyrrell, Lorne

APPLICANT: Tyrrell, Lorne

APPLICANT: Tyrrell, Lorne

TILE REFERENCE: 656.0016

CURRENT PRILICATION NUMBER: US/10/365,620

CURRENT FILING DATE: 2003-02-13

PRIOR PLILOM DATE: 2003-02-13

PRIOR PLILOM DATE: 2003-02-13

PRIOR PLILOM DATE: 2003-06-20

NUMBER OF SEQ ID NOS: 76

SOFTHARE: Patentin version 3.2

SEQ ID NO 56

LENGTH: 473
                                                           RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                      61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRKSRNLG 120
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93.4%; Score 976; DB 15; Length 473;
Best Local Similarity 92.7%; Pred. No. 2e-77;
Matches 177; Conservative 5; Mismatches 9; Indels
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121 KVIDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLA 180
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Patent No. US20020155582A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                181 LLSCLTTPASA 191
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LENGTH: 3011
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Patent No. US20020119495A1
GENERAL INFORMATION:
APPLICANT: HAWAII BIOTECHNOLOGY GROUP, Inc.
APPLICANT: NAKANO, Eileen
TITLE OF INVENTION: IMMUNOGENIC COMPOSITION OF HEPATITIS C
FILE REFERENCE: HAWBIOLIO
CURRENT APPLICATION NUMBER: US/09/952,572
CURRENT FILING DATE: 2001-09-13
PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                   Score 976; DB 9; Length 3011;
Pred. No. 1.5e-76;
5; Mismatches 9; Indels
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APPLICANT: Lemon, Stanley M.
ITILE OF INVENTION: Chimeric HCV/GBV-B viruses
FILE REFERENCE: 1D01116
CURRENT APPLLCATION NUMBER: US/09/742,659
CURRENT FILING DATE: 2000-12-21
FRIOR APPLICATION NUMBER: US 60/171,469
FRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 92.7%;
Matches 177; Conservative
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ORGANISM: Hepatitis C virus
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Best Local Similarity 92.7
Matches 177; Conservative
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Best Local Similarity
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LENGTH: 3011
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US-09-742-659-4
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APPLICANT: Lemon, Stanley
APPLICANT: Lemon, Stanley
APPLICANT: Yi, MinKyung
TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
FILE REPERBNCE: 265.0007 0101
CURRENT APPLICATION NUMBER: US/09/747,419
PRIOR APPLICATION NUMBER: US 60/171,909
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 34
SOSTWARE: PATENTIN VERSION 3.0
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93.4%; Score 976; DB 9; Length 30
Best Local Similarity 92.7%; Pred. No. 1.5e-76;
Matches 177; Conservative 5; Mismatches 9; Indels
Sequence 1, Application US/09929955
Patent No. US20020136740A1
GENERAL INPORMATION:
APPLICANT: Matti Sallberg
APPLICANT: Catharina Hultgren
TITLE OF INVENTION: WACTORES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: WACTORES CONTAINING RIBAVIRIN AND
TITLE REFERENCE: TRIPEP.23AUS2
CURRENT APPLICATION NUMBER: US/09/929,955
CURRENT FILING DATE: 2000-08-15
PRIOR PILING DATE: 2000-08-15
PRIOR PELING DATE: 2000-08-29
PRIOR PELING DATE: 2000-08-29
PRIOR PELING DATE: 2000-08-29
PRIOR PELING DATE: 2000-08-17
NUMBER OF SEC ID NOS: 49
SCOTWARE: FastSEQ for Windows Version 4.0
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Search completed: October 30, 2004, 01:49:51 Job time : 130 secs

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993.004 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                 protein search, using sw model
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AAR92982
AAR92984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR29539
AAR34470
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM50828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR92953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR34472
                                                                                                                     OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                              Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                              geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                         A_Geneseq_23Sep04:*
                                                                                                                                                                                                                                                            geneseqp1990s:*
                                                                                                                                                                                                                                                                                    geneseqp2002s:*
                                                                                                                                                                                                                                                                    geneseqp2000s:*
                                                                                                                                                                                                                                                                             geneseqp2001s:*
                                                                                                                                                                                                                                                                                                               geneseqp2004s:*
                                                                                   US-09-084-691B-206
                                                                                                                                                                                                seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyright
                                                                                                                                                                                                                                                                                                                                                                                                         100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226.7
226.7
226.7
226.7
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226.7
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                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                            Perfect score:
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                                 OM protein
                                                                                                                                                                                                Minimum DB
Maximum DB
                                                                                                                                                                                                                                          Database :
                                                                                                                                                             Word size
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                                                   on:
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Aar34478 Encoded 1	Aar34474 Encoded l	Aar34477 Encoded h	Aar34476 Encoded b	Aar34479 Encoded h	Aar34473 Encoded b	Aar34475 Encoded b	Aar34469 Encoded b	Aar34467 Encoded b	Aar34471 Hepatitis	Aam47263 Cuticle p	Aam47265 Cuticle p	Adj82984 Adenovect	Aar54067 Non-A, no	Aar98362 5'UTR/COR	Abg32458 Hepatitis				
AAR34478	AAR34474	AAR34477	AAR34476	AAR34479	AAR34473	AAR34475	AAR34469	AAR34467	AAR34471	AAM47263	AAM47265	ADJ82984	AAR54067	AAR98362	ABG32458	ABG32459	ABG32451	ABG32455	ABG32457
C)	N	7	ď	~	7	7	7	~	~	~	~	80	7	~	Ŋ	ស	2	ß	Ŋ
470	470	470	470	470	470	470	470	470	470	729	729	1026	1031	1031	3010	3010	3010	3010	3010
26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.7
51	21	51	51	21	51	21	21	51	51	51	21	21	21	51	21	21	51	51	21
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monomuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                       DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                        1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                core protein.
             AAR92987 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 223; 340pp; English
                                                                                                                                                                                                                                                                                                                                      Purcell RH;
                                                                                              Hepatitis C virus isolate HK2
                                                                                                                                                                                                                                                   95WO-US010398
                                                                                                                                                                                                                                                                              94US-00290665
                                                                                                                                                                                                                                                                                                          (USSH ) US SEC DEPT HEALTH
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-139709/14.
N-PSDB; AAT16661.
                                                                                                                                                                                                                                                                                                                                    Bukh J, Miller RH,
                                                                                                                        El; envelope
                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                           WO9605315-A2.
                                                                                                                                                                                                                                                   15-AUG-1995;
                                                                                                                                                                                                                                                                                15-AUG-1994;
                                                                  02-OCT-1996
                                                                                                                                                                                                                        22-FEB-1996.
                                                                                                                                     hepatitis.
                                     AAR92987;
AAR92987
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Score 191; DB 2; Length 191; Pred. No. 1.9e-167;

100.0%; 100.0%;

Query Match Best Local Similarity

Sequence 191 AA; HCV infection

71

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HCV; non-A, non-B hepatitis; NANBH; diagnosis; vaccine; antigen; antibody; immunoassay; assay; core protein.
Hepatitis C virus Jl isolate core protein.
                                                        AAW30597 standard; protein; 97
                                                                                             (first entry)
                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97 AA;
                                                                                                                                                                                                                                                               02-AUG-1993;
24-FEB-1994;
                                                                                                                                                                                                                   03-NOV-1994;
                                                                                                                                                                                                                                               11-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                              US5856437-A.
                                                                                                                                                                                                                                     15-SEP-1989;
                                                                                                                                                                                                                                                       04-JAN-1991;
                                                                                            10-MAY-1999
                                                                                                                                                                                                05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                              components
                                                                          AAW30597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
           21
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Matches
                                                AAW30597
                                       RESULT
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                                                                           120
                                                        61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
                                                                                                          KVIDTLICGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ79776 encodes AAR66633 the prod. of the hepatitis C virus (HCV) J1 core domain consensus sequence. They can be used to provide new oligonucleotides and polypeptides for use in diagnostics, recombinant protein prodn. and anti-HCV vaccine development. (Updated on 25-MAR-2003 to correct PF field.)
                      9
                                       09
                                                                      1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                  Method of detecting hepatitis C virus polynucleotide - utilises probe based on DNA of new HCV isolates J1 and J7.
    Gaps
                                                                                                                                                                                                                                                                                  Hepatitis C virus J1 core domain; anti-HCV vaccine development; non-A non-B virus; diagnostic polypeptides; HCV probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton M;
    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 26.7%; Score 51; DB 2; Length 97; 1 Similarity 100.0%; Pred. No. 8e-39; 51; Conservative 0; Mismatches 0; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolberg JA,
                                                                                                                                                                                                                                                                   Hepatitis C virus J1 core domain consensus protein.
    ..
0
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito I, Miyamura T, Cha T,
3D, Weiner AJ;
                                                                                                                                                                                                  AAR66633 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIRON CORP.

NAT INST OF HEALTH JAPAN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 18; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                      89US-00408045.
89US-00456142.
91US-00637380.
93US-00101280.
                                                                                                                                                                                                                                                                                                                                                                      94US-00201066.
                                                                                                                                                                                                                                       (revised)
(first entry)
    Matches 191; Conservative
                                                                                                                                    LLSCLTTPASA 191
                                                                                                                                                 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-030306/04.
                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ79776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1989;
04-JAN-1991;
02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1989;
                                                                                                                                                                                                                                      25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                  US5372928-A
                                                                                                                                                                                                                                                                                                                                                   13-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Han J, Sair
Irvine BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                            61
                                                                                               121
                                                                                                                                    181
                                                                                                                                                      181
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                                                                                                                                                                                        AAR66633
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This polypeptide comprises a core protein of novel Japanese isolate J1 of hepatitis C virus (HCV), as deduced from an amplified DNA clone (see AAX00458). The sequence shows homology to prototype HCV-1. The invention provides new Japanese isolates, J1 and J7, of HCV. The new isolates have nucleotide and amino acid sequences which are distinct from the prototype HCV-1 isolate. These differences can be exploited for use in diagnostics HCV-1 isolate. These differences can be exploited for use in diagnostics for NANDH, recombinant protein production and vaccine development.

Claimed antigenic polypeptides (see AAM30583-87) can be used: (i) as immunoassay reagents, or standards, to detect HCV antibodies, e.g. for diagnosing infection or screening donated blood; (ii) to generate specific antibodies (used for detecting the corresponding polypeptide, to screen for antiviral agents, for virus isolation and for passive immunisation); (iii) in protective or therapeutic vaccines, and (iv) for isolation of non-A, non-B viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                     Saito I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigenic polypeptides from J1 and J7 hepatitis C virus isolates as immunoassay reagents, for raising antibodies and as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .<del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.7%; Score 51; DB 2; Length 97; ilarity 100.0%; Pred. No. 8e-39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     Han J,
                                                                                                                                                                                                                                                                                                                                                     Kolberg JA,
                                                                                                                                                                                                                                                                                                                                                     Irvine BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Fig 18; 44pp; English.
                                                                                                                                                                                                                                                (NAHE-) NAT INST OF HEALTH JAPAN. (CHIR ) CHIRON CORP.
                                                         89US-00408045.
89US-00456142.
91US-00637380.
93US-00101280.
94US-00201066.
94US-00334255
                                                                                                                                                                                                                                                                                                                                                            Miyamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-105191/09.
N-PSDB; AAX00458.
                                                                                                                                                                                                                                                                                                                                                  Weiner AJ, Miyamura
Cha T, Houghton M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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Gaps

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Matches

Hepatitis C virus; HCV; screening; identification; non A non B hepatitis;

Hepatitis C virus.

NANBH

US5959092-A

28-SEP-1999

Hepatitis C virus Jl domain consensus amino acid sequence.

```
Immunoassays for Asiatic strains of hepatitis C virus - for diagnosis of infection and screening blood supplies.
                                                                         HCV; J7 isolate; J1 isolate; HCV1; immunoassay; asiatic strain; diagnosis; HCV infection; blood screening; immunisation; antiviral.
                                                          Protein encoded by HCV J1 untranglated and core domains.
        AAY01624 standard; protein; 97 AA
                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 18; 43pp; English.
                                                                                                                                                                                                                              (NAHE-) NAT INST OF HEALTH JAPAN. (CHIR ) CHIRON CORP.
                                                                                                                                                                            89US-00456142.
91US-00637380.
93US-00101280.
94US-00201066.
94US-00334255.
                                                                                                                                                     95US-00436965
                                          (first entry)
                                                                                                                                                                                                                                                        Miyamura T;
                                                                                                                                                                                                                                                                       1999-166619/14.
                                                                                                  Hepatitis C virus
                                                                                                                                                                                                                                                                       WPI; 1999-166619/
N-PSDB; AAX26743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97 AA;
                                          21-JUN-1999
                                                                                                                                                   08-MAY-1995;
                                                                                                                                                                             21-DEC-1989;
04-JAN-1991;
                                                                                                                                                                                             02-AUG-1993;
24-FEB-1994;
                                                                                                                                                                                                              03-NOV-1994;
                                                                                                                  US5871903-A
                                                                                                                                   16-FEB-1999
                                                                                                                                                                     15-SEP-1989;
                         AAY01624
                                                                                                                                                                                                                                                      Saito I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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26.7%; Score 51; DB 2; Length 97; 100.0%; Pred. No. 8e-39; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.7
Best Local Similarity 100.
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-AUG-2003
01-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM50828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is encoded by the consensus sequence of the untranslated and core domains of a new hepatitis C virus (HCV), J1. The J1 and J7 (also a new HCV isolate) isolates comprise sequences which are distinct from the prototype HCV isolates, HCV1. The specification cross-reactive with HCV-1. The assays are used for diagnosis of HCV infection and to screen donated blood. The anti-HCV antibodies are also useful therapeutically and prophylactically (passive immunisation); in screening for antiviral agents, for isolation, purification and indentification of non-A, non-B hepatitis virus (e.g. by affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification of non-A, non-B hepatitis virus (e.g. by affinity chromatography) and to raise anti-idiotypic antibodies (useful for treatment or diagnosis and to determine immunogenic regions of the HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 51; DB 2; Length 97; 100.0%; Pred. No. 8e-39; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF66080 standard; protein; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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51;

Best Loc Matches

g ð

12-FEB-2004 (first entry)

ADF66080;

RESULT 5
ADF66080
ID ADF6
XX
AC ADF6
XX
DT 12-F1

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71
                  71
               DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                              antigen; immunogen; infection; diagnosis; vaccine.
                                                                                                                                                                                   Location/Qualifiers
                                                             AAM50828 standard; protein; 120 AA.
                                                                                                                            Hepatitis C virus core antigen.
                                                                                                                                                                                                               10. .24
/label= MDL-2
                                                                                                                                                                                                                                28. .42
/label= MDL-3
                                                                                                                                                                                             1. .18
/label= MDL-1
                                                                                                            (first entry)
                                                                                                  (revised)
                                                                                                                                                                                          Peptide
                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                              Peptide
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. 0

Gaps

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Length 97;

The present invention describes polynucleotides sequences from Hepatitis C virus (HCV) isolates J7 C/E, J1 E, J1 E/NS1, J1 N33, and J1 NS5 or from deposits BP-2593, BP2594, BP-2595, BP-2637 and BP-2638. The polynucleotide sequences are useful as probes for screening and

identifying carriers of non A non B hepatitis (NANBH). The present sequence is used in the exemplification of the present invention.

Polynucleotide probes useful for screening and identifying carriers of non A non B hepatitis.

Example; Fig 18; 44pp; English.

CHIRON CORP.

NAT INST OF HEALTH JAPAN.

Miyamura T;

Saito I, (CHIR) ((NAHE-) N

WPI; 1999-570774/48. N-PSDB; ADF66079.

89US-00408045. 89US-00456142. 91US-00637380. 94US-00101280. 94US-00334255.

95US-00436966

08-MAY-1995;

21-DEC-1989;

04-JAN-1991

15-SEP-1989

03-NOV-1994; 02-AUG-1993; 24-FEB-1994;

control; proteolytic processing; precursor.

Hepatitis C virus.

EP518313-A2 16-DEC-1992

```
The present sequence is that of the core antigen (amino acids 1-120) of
the polyprotein encoded by hepatitis C virus (HCV). A panel of
c verlapping peptides between positions I and 186 of the HCV core region
was synthesised and tested for immunoreactivity with a commercially
c available human serum panel. All of the immunoreactivity was concentrated
within the region between amino acids I to 80. The invention provides a
confighly immunoreactive peptides MDL-1 to MDL-6 (see AAMS0816-27) from
c more of immunoreactive peptides MDL-1 to MDL-6 (see AAMS0816-27) from
this region of the core antigen. Each peptide is individually immobilised
to a carrier. The unique combination of HCV core peptides in the MAC
provides higher specificity and sensitivity for detection of human
antibodies specificity to HCV in rapid HCV diagnostic applications. An in
vitro diagnostic method for detecting anti-HCV antibodies in a test
sample and a diagnostic test kit are provided which use the MAC as an
immunoreagent. The HCV MAC may also potentially be used as an immunogen
in vaccine compositions. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                        New hepatitis C virus (HCV) peptides and mosaic antigen composition comprising the peptides, useful as immunoreagents for detecting HCV antibodies infection, or as an immunogen for stimulating production of antibodies against HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 59; 59pp; English.
                             48. .65
/label= MDL-5
                                                                                 /label= MDL-6
87. .101
                                                                                                                                         103. .120
/label= MDL-8
41. .57
/label= MDL-4
                                                                                                                      /label= MDL-7
                                                                                                                                                                                                                                                                   06-JUL-2001; 2001WO-CA000988
                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000CA-02311022
                                                                  66. .80
                                                                                                                                                                                                                                                                                                                                                                         Theolis R;
                                                                                                                                                                                                                                                                                                                                        (MEDM-) MEDMIRA INC.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-179696/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 120 AA;
                                                                                                                                                                                              WO200204484-A2
                                                                                                                                                                                                                                                                                                                                                                         Chan HKW,
                                                                    Peptide
                                                                                                       Peptide
Peptide
                                   Peptide
                                                                                                                                         Peptide
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New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.

Claim 5; Page 75-76; 305pp; English.

Hayashi N;

Teranishi Y,

Murakami T,

Takahashi K,

Honda Y,

Seki M,

WPI; 1992-417213/51. N-PSDB; AAQ32438.

(MITU) MITSUBISHI KASEI CORP.

91JP-00172794. 91JP-00287008. 91JP-00332329. 92JP-00099957.

11-JUN-1991; 12-JUL-1991; 07-OCT-1991;

16-DEC-1991; 20-APR-1992;

92EP-00109812 91JP-00139268

11-JUN-1992;

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The sequences given in AAR25929-30 and AAR29534-42 represent various clones of the polypeptide core-envelope region of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The RNA sequences encoding these pepitdes were converted into CDNA using transcriptase in the presence of one of the primer sequences given in AAQ32540-46. The CDNA sequences isolated represent different alleles of the same region of the HCV genement of a diagnostic method which is more accurate and effective than conventional ones, in the detection of antibodies raised against a conventional ones, in the detection of antibodies raised against a convention and in vitro screening system for a substance capable of specifically supressing or controlling a proteolytic processing of a precursor polypeptide of HCV. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    envelope 1; core protein; HCV genotyping; antibody; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 51; DB 2; Ld 100.0%; Pred. No. 1.3e-38; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus isolate T10 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR92948 standard; protein; 190 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9605315-A2
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0

Gaps

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26.7%; Score 51; DB 5; Length 120; 100.0%; Pred. No. 9.5e-39; ive 0; Mismatches 0; Indels

51; Conservative

Query Match Best Local Similarity Matches 51; Conserv

71

AAR29529 standard; protein; 170 AA

RESULT 7

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21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP

Clone; polypeptide; core-envelope; region; Hepatitis C; Virus; HCV; HC; cDNA; transcriptase; primer; allele; diagnostic; antibody; supress;

HCV core-envelope peptide N3-1.

(first entry)

(revised)

25-MAR-2003 26-APR-1993

AAR29529;

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Purcell RH;

used ö 0

Gaps

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71

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AAR92936-R92987 are HCV core proteins derived from 52 different HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 191 AA
                         95WO-US010398,
                                                                             94US-00290665
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                                                                                                                                (USSH ) US SEC DEPT HEALTH
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                                                                                                                                                                                     Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miller RH,
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Best Local Similarity
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                                                                                                                                                                                                                                                                  N-PSDB; AAT16622
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                         15-AUG-1995;
                                                                             15-AUG-1994;
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$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
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26.,; 100.0%; Pr

26.78;

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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
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isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           El; envelope 1; core protein; HCV genotyping; antibody; vaccine;
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                                                                                                                                                                                                                 Length 191;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                             DB 2; Le
1.4e-38;
                                                                                                                                                                                                          26.7%; Score 51; DB 100.0%; Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR92983 standard; protein; 191 AA
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                                                                                                                                                                                                                                Local Similarity
nes 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                        Sequence 191 AA;
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                                                                                                                               HCV infection
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Matches
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                                                                                                                                                                                                                                                      used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
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                                                                                                                                                                                                                                                 DNA and amino acid sequence of HCV envelope 1 and core proteins determine HCV genotype and as vaccines against HCV infection.
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Gaps

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Purcell

AAR92979 standard; protein; 191 AA.

RESULT 11

(first entry)

02-OCT-1996

AAR92979;

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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                        isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the CDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                  DNA and amino acid sequence of HCV envelope 1 and core proteins - used determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                          AAR92936-R92987 are HCV core proteins derived from 52 different HCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.7%; Score 51; DB 2;
100.0%; Pred. No. 1.4e-3:
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus isolate SA5 core protein.
                                                                                                                                                                                                                                                                           Claim 4; Page 196-197; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR92980 standard; protein; 191 AA.
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                                                                                                                                    Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US010398.
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                                95WO-US010398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US SEC DEPT HEALTH
                                                                                                  (USSH ) US SEC DEPT HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1996-139709/14
                                                                                                                                    Miller RH,
                                                                                                                                                                     WPI; 1996-139709/14.
N-PSDB; AAT16629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT16654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1994;
                                15-AUG-1995;
                                                                 15-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9605315-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-1996
22-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR92980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukh J,
                                                                                                                                      Bukh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                         envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; Le
Pred. No. 1.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.7%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus isolate HK4 core protein.
                                                                                                                                                        Hepatitis C virus isolate SA4 core protein.
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Claim 4; Page 216-217; 340pp; English.

Purcell RH;

Miller RH,

Bukh J,

WPI; 1996-139709/14

N-PSDB; AAT16653

(USSH) US SEC DEPT HEALTH.

95WO-US010398 94US-00290665

15-AUG-1995; 15-AUG-1994;

Hepatitis C virus.

hepatitis.

WO9605315-A2 22-FEB-1996. AAR92955 standard; protein; 191 AA

RESULT 12

02-OCT-1996

Hepatitis C virus.

hepatitis

HCV;

WO9605315-A2

Conservative

51;

Matches

ò g

Query Match Best Local Similarity

Sequence 191 AA; HCV infection

. 0

ζQ

envelope 1; core protein; HCV genotyping; antibody; vaccine;

Hepatitis C virus.

hepatitis E1;

WO9605315-A2

22-FEB-1996.

Hepatitis C virus isolate SA10 core protein.

02-OCT-1996

AAR92942;

AAR92942 standard; protein; 191 AA.

RESULT 15 AAR92942

<u>_</u>

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·;
AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monomuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCV; E1; envelope 1; core protein; HCV genotyping; antibody; vaccine;
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                     DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                                                           Length 191;
                                                                                                                                                                                                        0; Indels
                                                                                                                                                                          DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus isolate SA7 core protein.
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                          Score 51;
Pred. No.
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                                                                                                                                                             26.7%; Scu-
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 218; 340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RH;
                                                                                                                                                                                                                                                                                                                                             AAR92981 standard; protein; 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US010398,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-00290665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purcell
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                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-139709/14
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT16655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 191 AA;
                                                                                                                                           Sequence 191 AA;
                                                                                                            HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9605315-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-1996.
                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis.
                                                                                                                                                                                                                                                                                                                                                                             AAR92981;
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                                                                                                                                                                                                        Matches
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RH;

Purcell

Miller RH,

Bukh J,

WPI; 1996-139709/14.

N-PSDB; AAT16616

95WO-US010398.

15-AUG-1995; 15-AUG-1994;

94US-00290665

(USSH) US SEC DEPT HEALTH

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0
                                                                                                                                                                                                                                                                                                                              DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                     AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated DNA sequences are used for the prodn. of primers useful for detecting the predence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunishing against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other monopurclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.7%; Score 51; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Preα....
                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 185-186; 340pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Search completed: October 30, 2004, 01:53:46 Job time : 70 secs

ö

Gaps

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Length 191;

1.4e-38;

Score 51; DB 2; Pred. No. 1.4e-3

26.78;

100.0%; Pred. w..

Conservative

Local Similarity

Query Match

51;

Best Loc Matches

21

à 원

DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71

DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP

```
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
```

OM protein - protein search, using sw model

October 30, 2004, 01:49:56 ; Search time 16 Seconds (without alignments) 1148.588 Million cell updates/sec Run on:

US-09-084-691B-206

191 1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191 Perfect score:

Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

Searched:

0 Word size :

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 07 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	genome polyprofein						genome polyprotein														genome polyprotein		_	genome polyprotein					
	ID	S41362	S41370	S18032	S18031	S19875	PN0677	S18030	S41371	S41365	PQ0804	S41341	S4136B	S41366	841350	S41351	S41343	S41345	S41364	S41363	S41346	JN0265	S12707	A44150	JQ1584	GNWVCJ	GNWVC3	GNWVCH	S21336	841357
	DB	2	~	α	~	7	7	П	N	7	~	7	~	~	7	~	7	7	~	7	~	~	7	7	7	-	Н	н	7	7
	Length	114	114	782	782	782	787	3010	112	114	82	112	114	114	115	115	115	115	115	117	118	322	441	513	640	3010	3011	3011	88	108
æ	Query Match	26.7	26.7	26.7	26.7	26.7	26.7	26.7	26.2	26.2	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	25.7	24.6	24.6
	Score	51	51	51	51	51	51	51	20	20	49	49	49	49	49	49	49	49	49	49	49	4.9	49	49	49	49	49	49	47	47
	Result No.	1	7	m	4	ഹ	9	7	c o	o,	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	29

genome polyprotein			genome polyprotein	polyprotein - hepa	genome polyprotein	genome polyprotein	core protein - hep	genome polyprotein	genome polyprotein	genome polyprotein				
S41356 S41355	841353	S41354	JQ0883	JQ0881	S40770	GNWVJ8	JQ1303	S32740	S21471	PC1284	PQ0805	S41352	S41349	S41358
0.0	1 (7)	N	7	N	Н	Н	Н	N	7	N	N	7	~	7
108	108	115	874	874	3011	3033	3033	189	369	513	75	125	115	114
24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	22.0	21.5	20.9	19.9	19.4	18.3	17.8
47	47	47	47	47	47	47	47	42	41	40	38	37	35	34
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
N; Contains: core protein
C; Species: hepatitis C virus
A; Variety: genotype 4, NI
C; Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C; Accession: 541362
R; Van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A; Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A; Reference number: 541341
A; Accession: 541362
A; Molecule type: genomic RNA
A; Residues: 1-114 < VAN>
A; Reperimental source: genotype 4, NI
C; Superfamily: hepatitis C Virus genome polyprotein
C; Reywords: capsid protein; core protein; polyprotein
F; 1-114/Product: core protein #status predicted < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                     polyprotein - hepatitis C virus (genotype 4, N1) (fragment)
RESULT 1
S41362
genome 1
N; Contai
```

.; 0 ch 26.7%; Score 51; DB 2; Length 114; 1 Similarity 100.0%; Pred. No. 7.5e-43; 51; Conservative 0; Mismatches 0; Indels Query Match Best Local Si Matches 51

21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71 21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71 à 셤

Genome polyprotein - hepatitis C virus (genotype 5, N4) (fragment)
N;Contains: core protein
C;Specias: hepatitis C virus
A;Variety: genotype 5, N4
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: \$4130.
R;Van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
Submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: \$41310
A;Reference number: \$41310
A;Recession: \$41370
A;Residues: 1-114 <VANA
A;Residues: 1-114 <VANA
A;Resperimental source: genotype 5, N4
C;Superimental source: genotype 5, N4
C;Superimental source: genotype 5, N4
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capaid protein; core protein; polyprotein
F;1-114/Product: core protein #status predicted <MAT>

Query Match

26.7%; Score 51; DB 2; Length 114;

```
A;Variety: isolate JK3
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19875
R;Honda, M.; Kanekc, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus isolatefacence number: S18029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Crose-references: UNIPROT:Q68951; EMBL:X61592; NID:g59482; PIDN:CAA43789.1; PID:g59483
A;Crose-references: UNIPROT:Q68951; EMBL:X61592; NID:g59482; PIDN:CAA43789.1; PID:g59483
A;Experimental source: isolate UX3
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted <MAT2>
F;384-733/Product: nonstructural #status predicted <MAT3>
F;384-733/Product: nonstructural protein 2 (fragment) #status predicted <MAT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q08244; GB:L20498; NID:g1381031; PIDN:AAB02608.1; PID:g1381
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Variety: isolate JK1
C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C; Accession: S18030; S33570; A4832; S18029
R; Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A; Description: A whole genome of hepatitis C virus cDNA was isolated from a single pati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (nonstruct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies hepatitis C virus Cibbre 1994 #text_change 09-Jul-2004 Cibbre: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004 Cibbre: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004 Cibbresion: PN0677 Jil Chang, JE.; Ahn, B.M.; Lee, C.H.; Lee, Y.I. Biochem. Biophys. Res. Commun. 196, 780-788, 1993 A;Tile: Genomic typing of hepatitis C viruses from Korean patients: Implications of A;Reference number: PN0677; MUID:94059104; PMID:8240354
                                                                                                 N; Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein C; Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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N.Contains: capsid protein C, envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.7%; Score 51; DB 2; Length 782; 100.0%; Pred. No. 3.6e-42; ive 0; Mismatches 0; Indels
                                                                                     (fragment)
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                                                                                     JK3)
                                                                                         (isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.7%;
                                                                                             hepatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: genomic RNA
A;Residues: 1-782 <HON>
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A;Molecule type: mRNA
A;Residues: 1-787 <CHO>
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C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Accession: 318032
R; Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A; Description: Sequence analysis of putative structural regions of Hepatitis C Virus isc
A; Reference number: 318029
A; Accession: S18032
A; Accession: S18032
A; Accession: S18032
A; Accession: S18032
A; Accession: Sladon ENNA
A; Residues: 1-702 - 4HON>
A; Residues: 1-702 - 4HON>
A; Residues: 1-702 - 4HON>
A; Essidues: 1-703 - 4HON>
A; Essidues: 1-704 - 4HON>
A; Essidues: 1-705 - 4HON>
A; Essidues: 1-705 - 4HON>
A; Essidues: 1-705 - 4HON>
A; Essidues: 1-706 - 4HON>
A; Essidues: 1-706 - 4HON>
A; Essidues: 1-708 - 4HON>
A; Essidues: 1-70
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R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
Bubmitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of Hepatitis C Virus isc
A;Reference number: S18029
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Subperfamily: hepatitie C virus genome polyprotein
C;Superfamily: hepatitie C virus genome polyprotein; glycoprotein; nonstructural
C;Keywords: capsid protein; core protein; envelope protein; glycoprotein; nonstructural
F;1-191/Product: core protein #status predicted <MAT1>
F;392-393/Product: envelope protein; #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted <MAT4>
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N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                     genome polyprotein - hepatitis C virus (isolate JK4) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
C;Species: hepatitis C virus
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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100.0%; Pred. No. 3.6e-42;
ive 0; Mismatches 0;
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Pred. No. 3.6e-42;
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7.5e-43;
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A;Residues: 1-782 <HON>
A;Cross-references: UNIPROT:Q68950; EMBL:X61593
                             Mismatches
Pred. No.
                             0;
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Cyspecies: hepatitis C virus (fragment)
Cyspecies: hepatitis C virus
Cyspecies: p00804
Rysimmonds, P.; McOmish, F.; Yap, P.L.; Chan, S.W.; Lin, C.K.; Dusheiko, G.; Saeed, A.A.
J. Gen. Virtol. 74, 661-668, 1993
A.; Title: Sequence variability in the S' non-coding region of hepatitis C virus: identifi
A; Reference number: p00803; MulD: 93224886; PMID: 8385694
A; Accession: p00804
A; Molecule type: mRNA
A; Residues: 1-82 <SIMA
A; Residues: 1-82 
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A,Molecule type: genomic RNA
A,Residues: 1-114 < VANA
A,FResidues: 1-114 < VANA
A,Cross-references: UNIPROT:068899; EMBL:Z29468; NID:g443898; PIDN:CAA82606.1; PID:g4438
A,Experimental source: genotype 4, N4
A,Experimental source: genotype 4, N4
C,Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; polyprotein
F;1-114/Product: core protein #status predicted <NAT>
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                         genome polyprotein - hepatitis C virus (genotype 4, N4) (fragment)
N;Contains: core protein
C;Species: hepatitis C virus
A;Variety: genotype 4, N4
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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N;Contains: core protein
N;Contains: core protein
A;Species: hepatitis C virus
A;Variety: genotype 1, NI
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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5.5e-41;
hes 0; Indels
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R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to
A;Reference number: S41341
A;Accession: S41365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.7%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
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R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Conservative
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Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
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S41341
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; F:2-115/Product: capsid protein C #status predicted <CPC>
F:16-191/Product: envelope protein C #status predicted <CPM>
F:192-389/Product: envelope protein E #status predicted <MED>
F:390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F:1007-1615/Product: hepacivirin #status predicted <NS2>
F:1230-1231/Region: nucleotide-binding motif B (P-loop)
F:1317-131/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 File16-1862/Product: nonstructural protein NS4a #status predicted <N4A>
Fil863-2013/Product: nonstructural protein NS4b #status predicted <NB>
Fil863-2013/Product: nonstructural protein NS4b #status predicted <NS5>
Fil864-3010/Product: nonstructural protein NS5 #status predicted <NS5>
Fil96,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (Ag
                                                                                                             A.Cross-raferences: UNIPROT:068949; EMBL:X61596; NID:959478; PIDN:CAA43793.1; PID:959479
A;Experimental source: isolate JK1 from an individual
                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: genomic RNA
A;Residues: 1-547,'T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOW>
A;Cross-references: ENBL:X61591
A;Note: this sequence is anconsistent with the nucleotide translation
A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TTC for residue 771 as Ser
A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)
                                                                                                                                                       A, Experimental source: isolate JK1 from an individual
R; Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A,Title: Sequence analysis of putative structural regions of hepatitis C virus isolated A, Reference number: A48332; MUID:93119270; PMID:8380322
A, Accession: S33570
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Nicontains: ore protein
Cispecies: hepatitis C virus
A;Variety: genotype 5, N5
Cibate: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
Cipaccession: 541371
R;van Doorn, LJ; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: S41371
A;Accession: 541371
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A;Experimental source: genotype 5, NS
C;Superfamily: hepatitis C virus genome polyprotein
C;Steywords: capaid protein; core protein; polyprotein
F;1-112/Product: core protein #status predicted <MAT>
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Matches 51; Conservative
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Best Local Similarity 100.
Matches 50; Conservative
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A; Residues: 1-112 < VAN>
                                 A, Molecule type: genomic RNA
A, Residues: 1-3010 <HON>
S18030
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Query Match

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A, Cross-references: UNIPROT: Q68884; EMBL: Z29453; NID: 9443868; PIDN: CAA82591.1; PID: 94438
                                                                                                                                                                                                                                                         N.Contains: core protein
C.Species: heparitis C virus
A.Variety: genotype 1, N8
C.Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C.Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C.Accession: 841350
R.Van Doorn, L.J., Kleter, G.E.M.; Brouwer, J.T.
R.Van Doorn, L.J., Kleter, G.E.M.; Brouwer, J.T.
A.Pescription: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A.Reference number: 841341
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     Gaps
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A;Variety: genotype 1, N9
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul
C;Accession: 341351
R;Van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
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                                                                                                                                                                                                                                    genome polyprotein - hepatitis C virus (genotype 1, N8) (fragment)
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C.Superfamily: hepatitis C virus genome polyprotein
C.Keywords: capsid protein; core protein; polyprotein
F:1-115/Product: core protein #status predicted «MAT»
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A,Readidues: 1-115 <VNA
A,Cross-references: UNIPROT:068885; EMBL:229454
A,Experimental source: genotype 1, N9
C,Superfamily: hepatitis C virus genome polyprotein
C,Keywords: capsid protein; core protein; polyprotein
F;1-115/Product: core protein #status predicted <MAT>
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     Mismatches
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49; Conservative
     49; Conservative
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A; Residues: 1-115 < VAN>
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C;Species: hepatitis C virus

A;Variety: genorype 4, NS

C;Species: hepatitis C virus

A;Variety: genorype 4, NS

C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: 841366

R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.

submitted to the EMBL Data Library, January 1994

A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.

A;Reference number: 841361

A;Residues: 1-114 < VAN.

A;Residues: 1-114 < VAN.

A;Residues: UNIPROT: Q68900; EMBL: Z29469; NID: 9443900; PIDN: CAA82607.1; PID: 94439

A;Experimental source: genotype 4, NS

C;Superfamily: hepatitis C virus genome polyprotein

C;Keywords: capsid protein; core protein; polyprotein

F;1-114/Product: core protein #status predicted < MAT>
                                                                                                   A;Residues: 1-112 <VAN>
A;Cross_references: UNIPROT:Q68875; EMBL:Z29444; NID:g443850; PIDN:CAA82582.1; PID:g4438
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A, Cross-references: UNIPROT: Q68902; EMBL: Z29471; NID: G443904; PIDN: CAA82609.1; PID: G4439
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C;Species: hepatitis C virus
A;Variety: genotype 5, N2
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
     5 by LiPA
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A; Description: Analysis of hepatitis C virus genotypes 1 to A; Reference number: S41341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome polyprotein - hepatitis C virus (genotype 5, N2)
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                                                                                                                                                         A;Experimental source: genotypel, N1
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; polyprotein
F;1-112/Product: core protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                    25.7%; Score 49; DB 2; Le 100.0%; Pred. No. 7.1e-41; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Experimental source: genotype 5, N2
C'Shuperfamily: hepatitis C virus genome polyprotein
C'Keywords: capsid protein; core protein; polyprotein
C'Heywords: capsid protein #status predicted «MAT»
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Pred. No. 7.2e-41;
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A;Accession: S41368
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A, Molecule type: gen
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1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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26.77 26.77	PRELIMINARY;	(TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 24, (Fragment).	C virus. ssRNA positive-strand viruses, us. D=11103;	SEQUENCE FROM N.A. MEDLINE=94336721; PubMed=8058787; Bukh J., Purcell R.H., Miller R.H "Sequence analysis of the core ges genctypes."; Proc. Natl. Acad. Sci. U.S.A. 91:	PubMed PubMed R.H., M s of th	SEQUENCE FROM N.A. MEDLINE=93376778; PubMed=8356266; MEDLINE=93376778; PubMed=8356266; MAL Heast 12 genotypes of hepatitis C vianlysis of the putative El gene of isolero. Natl. Acad. Sci. U.S.A. 90:8234-88. Proc. Natl. Acad. Sci. U.S.A. 90:8234-88. GO: GO: 0019028; Caviral capsid; IEA.	D:0005198; F:structura Pro; IPR00252; HCV ca Pro; IPR002521; HCV co Pr01542; HCV capsid; Pr01542; HCV core; 1. rotein. 1 >191 ER 191 AA; 20725 M	,
32 33 34 34 34 35 36 37 37 38 44 42 41 51 44 51 44 51 51 44 51 51 51 51 51 51 51 51 51 51 51 51 51	LT 1 15 068115	11996 -1996 -2003 otein	hepatitis C viru Viruses; ssRNA po Hepativirus. NCBI_TaxID=11103	SEQUENCE FROM N.A. MEDLINE=94336721; Bukh J., Purcell R "Sequence analysis genotypes."; Proc. Natl. Acad.	[2] SEQUENCE FROM N.A MEDLINE=92279243, Bukh J., Purcell "Sequence analysi Proc. Natl. Acad.	SEQUENCE FROM N.A. MEDLINE=93376778; Bukh J., Purcell R "At least I genor analysis of the pu Proc. Natl. Acad. EMBL; U10198; AAAZ GO; GO:001908; CA	GO; GO:00051 InterPro; IP InterPro; IP Pfam; PF0154 Pfam; PF0154 Polyprotein. CHAIN NON TER SEQUENCE 1	
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                                 KVIDTLITCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                     KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
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SEQUENCE FROM N.A.
MEDLINE=96005057; PubMed=7561773;
Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K.,
                                                                                                                                                                                                                                                                                                                                                                                                                           84.3%; Score 161; DB 2; Length 191; 100.0%; Pred. No. 6.4e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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J. Clin. Microbiol. 34:2815-2818(1996).
R. BMBL, 1033435; AAB400301.;
GO; GO:0019028; C:viral capsid; IEA.
R. GO; GO:005198; F:structural molecule activity; IEA.
R. HICEPTO: IPR002522; HCV_capsid.
R. InterPro; IPR002521; HCV_capsid.
R. Pfam; PF01543; HCV_capsid; 1.
P. Fam; PF01542; HCV_core; 1.
P. Ram; PF01542; HCV_core; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                       191 AA; 20789 MW; F292AB64B56DE30A CRC64;
                                                                                                                                                Q68411;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Core protein (Freqment).
Hepatitis C virus type 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 161; Conservative
                                                                            PRELIMINARY;
                                                               181 LLSCLTTPASA 191
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11103;
                                                                                                                                                                                                                        Hepacivirus.
NCBI_TaxID=42182;
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76 WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLGKVIDTLTCGFADLMG 135
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Chainuvati T., Iizuka H., Tsuda F., Miyakawa Y., Mayumi M.; "Hepatitis C virus variants from Thailand classifiable into five novel genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b,\ 9c) major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   five novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 YIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLALLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
NON_TER 414 414
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Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 414;
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genetic groups.";

J. Gen. Virol. 76.2329-2335(1995).

EMBL; D37844; BAA07090.1;

GO; GO: 0019021; C: integral to membrane; IEA.

GO; GO: 0019021; C: viral capsid; IEA.

GO; GO: 0019031; C: viral envelope; IEA.

GO; GO: 0019031; C: viral envelope; IEA.

GO; GO: 0019031; C: viral envelope; IEA.

InterPro; IPR002521; HCV_capsid.

InterPro; IPR002521; HCV_capsid.

InterPro; IPR002531; HCV_capsid.

InterPro; IPR002531; HCV_env.

IPEam; PP01542; HCV_core.

PFam; PP01560; HCV_env; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 116; DB 2; Le
Pred. No. 2.5e-105;
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100.0%; Pred. No. ...
0; Mismatches
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Hepatitis C virus.
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Gaps

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AC 07503
AC 07503
BD 05-JU
DT 05-JU
DT 05-JU
DE HEPAR
COC VITAL
COC NCBL
LI 1
RR SEQU
RA HITAR
DR EMBL
DR EMBL
DR EMBL
DR FARM
EWW PT
RW NON'
SQ SEQUI

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21 DVKPPGGGIVGGVYLLPRKGPRLGVRATRKTSERSQPRGRRQPIPKARQPQSRHWAQPG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=VT315;
Hirano M., Tran H.T., Abe K.;
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
"Genotypic distribution of systems for identification of Vietnamese
HCV isolates.";
                                                                                         21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPQGRHWAQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPQGRHWAQPG
                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus; Hepatitis C virus type 6.
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Hepacivirus; Hepatitis C virus; Hepatitis C virus type 6.
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                     DB 2; Length 117;
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                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A. Abe K.;
SEQUENCE FROM N.A. Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ABL62864; BAD11958.1; -.
InterPro; IPR002522; HCV capsid.
Pfam; PF01543; HCV_capsid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB162864; BAD11958.1; -.
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117 AA; 13407 MW; 3EAE29D8CAE789F6 CRC64;
                                                                                                                                                                                                                                                                                                    075033;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                             81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                                                                                                                                                   81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
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                                        4.6e-87;
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                    50.8%; Score 97; DB 100.0%; Pred. No. 4.6 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Polyprotein (Fragment).
Hepatitis C virus type 6a.
                  Query Match
Best Local Similarity 100.
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus type 6a.
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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nes 97; Conserv
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03-MAR-2004 (
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SEQUENCE
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BAD11958;
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Matches
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                                                                                                      76 WAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLGKVIDTLTCGFADLMG 135
                                                                                                                            DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPGRHWAQPG 80
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Hepacivirus, Hepatitis C virus type 6.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Hepatitis C virus type 6.
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                                                                                                                                                                                            136 YIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLAL 181
                                      Length 414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Hirano M., Tran H.T., Abe K.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, ABL62667; BAD11561.1;
InterPro; IPR002522; HCV_capsid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Hirano M., Tran H.T., Abe K.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, ABLG2866: BAD11960.1;
InterPro, IPR002522; HCV capsid.
Pfam; PF01543; HCV_capsid, 1.
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SEQUENCE 117 AA; 13441 MW; 9EA99F0E118A3F20 CRC64;
45072 MW; 6C9E1AFE4642241D CRC64;
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117 AA; 13407 MW; 3EAE29D8CAE789F6 CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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                                  55.5%; Score 106; DB 2; I inlarity 100.0%; Pred. No. 1.7e-95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.8%; Score 97; DB 2; Le
100.0%; Pred. No. 4.6e-87;
tive 0; Mismatches 0;
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Best Local Similarity
   414 AA;
                                                 Local Similarity
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NON TER 1
SEQUENCE 11
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05-JUL-2004
05-JUL-2004
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05-JUL-2004
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                                                                     Matches 106;
 SEQUENCE
                                    Query Match
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075031

RESULT 6 Q75Q31

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9EA99F0E118A3F20 CRC64;
                                13441 MW;
                                                        50.8%;
EMBL; AB162867; BAD11961.1;
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Best Local Similarity 100.0
Matches 86; Conservative
                                                                Best Local Similarity 100.
Matches 97; Conservative
                                                                                                                                                                                                                               PRELIMINARY;
                         117
                                 117 AA;
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                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11103;
             Polyprotein.
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                                  SEQUENCE
                                                          Query Match
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                                                                      21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPQGRHWAQPG 80
                                                                                  STRAIN=VT657;
Hirano M., Tran H.T., Abe K.;
Hirano M., Tran H.T., Abe K.;
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
City, Vietnam: New genotyping systems for identification of Vietnamese
HCV isolates.";
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Hirano M., Tran H.T., Abe K.;
"Genotypic distribution of hepatitis C virus (HCV) in Ho Chi Minh
City, Vietnam: New genotyping systems for identification of Vietnamese
HCV isolates.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
Polyprotein (Fragment).
Heparitis C virus type 6a.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Heparitis C virus; Hepatitis C virus type 6.
NCBI_TaxID=31655;
                                                                                                                                                                                                                                                       Polyprotein (Fragment).
Hepatitis C virus type 6a.
Viruses; sRNA positive strand viruses, no DNA stage; Flaviviridae;
Hepatovirus; Hepatitis C virus; Hepatitis C virus type 6.
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Pred. No. 4.6e-87;
                         Length 117;
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                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB162866; BAD11960.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                              117 117
117 AA; 13407 MW; 3EAE29D8CAE789F6 CRC64;
   13407 MW; 3EAE29D8CAE789F6 CRC64;
                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
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                                                                                                                                 81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                                                                                  81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                          50.8%; Score 97; DB 2; Le
100.0%; Pred. No. 4.6e-87;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                 117 AA
                                     100.0%; Pred. No. 4.6
ive 0; Mismatches
                                                                                                                                                                                                                        Created)
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                97; Conservative
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                                                                                                                                                                                                  PRELIMINARY;
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     117 AA;
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=31655;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein.
NON TER
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03-MAR-2004
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It Submitted (AUG-1996) to the EMEL/GenBank/DDBJ databases.

BRBL; DB846; BAA13618.1; -..

BRBL; DB846; BAA13618.1; -..

BRBL; DB846; BAA13618.1; -..

BR GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR00252; HCV capsid.

InterPro; IPR00251; HCV enve.

R InterPro; IPR00251; HCV enve.

R InterPro; IPR00251; HCV enve.

R InterPro; IPR002531; HCV core.

R Pfam; PF01543; HCV capsid; 1.

R Pfam; PF01545; HCV NG1; 1.

R Pfam; PF01564; HCV NG1; 1.

R Pfam; PF01565; HCV NG1; 1.

R Pfam; PF01566; HCV NG1; 1.

R Pfam; FF01566; 
                                                                                                                                                                                                       21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPGGRHWAQPG 80
                                                                                                                                                                                                                                                                                                        21 DVKFPGGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQPGRHWAQPG 80
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Length 117;
                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 YPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSR 117
                                                100.0%; Pred. No. 4.6e-87; ive 0; Mismatches 0;
          Score 97; DB 2;
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Hepatitis C virus.
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MEDLINE=95062197; PubMed=7972001;
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Best Local Similarity
[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01560; HCV_NS1; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.

NON_TER 414 414 414
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Hepacivirus.
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Tokita H., Okamoto H., Tsuda F., Song P., Nakata S., Chosa T.,
Iizuka H., Mishiro S., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Vietnam are classifiable into the seventh, eighth, and ninth major genetic groups.";
Proc. Natl. Acad. Sci. U.S.A. 91:11022-11026(1994).
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100.0%; Pred. No. 8.4e-75;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic groups.";
J. Gen. Virol. 76:2329-2335(1995).

E.MBL; D37843; BAA070891;
GO; GO:0010021; C.:ntegral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:00019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

R InterPro; IPR002521; HCV capsid.

R InterPro; IPR002521; HCV env.

R InterPro; IPR002531; HCV env.

R InterPro; IPR002531; HCV env.

R InterPro; IPR002531; HCV capsid.

R Pfam; PF01542; HCV capsid; 1.

R Pfam; PF01542; HCV core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 AA; 44836 MW; 212740491A9DA0B1 CRC64;
                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Core, env and part of E2/NS1 (Fragment).
                                                                     414 AA
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                                                                                                                                                                                       Core, env, and part of E2/NS1 (Fragment).
Hepatitis C virus.
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                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=11103;
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Q81329;
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               RESULT 12
081268
10 081268
AC 081266
DT 01-UJU
DT 01-UJU
DE COTE,
OC HEPAC,

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107 WGPNDPRRKSRNLGKVIDTLITCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYAT 166
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"The entire nucleotide sequences of three hepatitis C virus isolates

"The entire groups"."

"The entire groups"."

"The other eight

"The ot
                                                                                                                                      A GO:0016021; EVUCUU4.

R GO: GO:0016021; C:integral to membrane; IEA.

GO: GO:0019028; C:viral capsid; IEA.

R GO: GO:0019028; C:viral capsid; IEA.

R GO: GO:0019031; C:viral capsid; IEA.

R GO: GO:0019031; C:viral capsid; IEA.

R GO: GO:005198; F:structural molecule activity; IEA.

R InterPro; IPR002521; HCV_core.

R InterPro; IPR002521; HCV_core.

R InterPro; IPR002531; HCV_core.

R InterPro; IPR002531; HCV_env.

R Pfam; PR01543; HCV_core.

R Pfam; PR01543; HCV_core.

R Pfam; PR01543; HCV_core.

R Pfam; PR01560; HCV_NS1.

R Pfam; PR01550; HCV_NS1.

R Pfam; PR01550; HCV_NS1; 1.

R Pfam; PR01550; HCV_NS1; 1.
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MEDLINE=98378034; PubMed=9714232;
Tokita H., Okamoto H., Iizuka H., Kishimoto J., Tsuda F., Miyakawa Y.,
Mayumi M.;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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100.0%; Pred. No. 8.4e-75;
ive 0; Mismatches 0; Indels
Okamoto H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                               EMBL; D88468; BAA13617.1; -. PIR; PQ0804; PQ0804.
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Search completed: October 30, 2004, 01:59:29 Job time : 68 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 WGPNDPRRRSRNLGKVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYAT 166
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Tokita H., Okamoto H., Luengrojanakul P., Vareesangthip K.,
Chainuvati T., Iizuka H., Tsuda F., Miyakawa Y., Mayumi M.;
"Hepatitis C virus variants from Thailand classifiable into five novel
genotypes in the sixth (6b), seventh (7c,7d) and ninth (9b, 9c) major
genetic groups.";
J. Gen. Virol. 76:232-2335(1995).
BME, D37846; BAA07092.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0019031; C:viral capsid; IEA.
GO, GO:0019031; C:viral envelope; IEA.
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Core, env and part of E2/NS1 (Fragment).
Hepatitis C virus.
GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019087; P:viral transformation; IEA.
InterPro; IPR0003415; CytC heme_BS.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002519; HCV core.
InterPro; IPR002519; HCV env.
InterPro; IPR002519; HCV MS1.
InterPro; IPR002519; HCV MS1.
InterPro; IPR001459; HCV MS2.
InterPro; IPR001490; HCV MS4.
InterPro; IPR001490; HCV MS5a.
InterPro; IPR001490; HCV ROSA.
InterPro; IPR001490; HCV ROSA.
InterPro; IPR001409; Peptidase_S29.
InterPro; IPR001003; Pept_SPC_VS.
InterPro; IPR001091; Pept_SPC_VS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.5%; Score 85; DB 2; Le 100.0%; Pred. No. 4.1e-74; Atlive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE=96005057; PubMed=7561773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | PF01539; HCV env. | PF01539; HCV env. | PF01560; HCV NS1; | 1. | PF01580; HCV NS2; | 1. | PF01580; HCV NS3; | 1. | PF01006; HCV NS4; | 1. | PF01001; HCV NS4b; | 1. | PF01001506; HCV NS5a; | 1. | PF01506; HCV NS5a; | 1. | PF000998; Viral_RdRP; | 1. | PF000998; Viral_RdRP; | 1. | PF01506; HCV NS5a; | 1. | PF000998; Viral_RdRP; | 1. | PF01506; HCV NS5a; | 1. | PF000998; Viral_RdRP; | 1. | PF01506; HCV NS5a; | 1. | PF000998; Viral_RdRP; | 1. | PF01506; HCV NS5a; | 1. | PF01506; HCV N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01543; HCV capsid;
PF01542; HCV core; 1.
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Best Local Similarity 100.
Matches 85, Conservative
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NCBI_TaxID=11103;
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InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_env.
InterPro; IPR002531; HCV_capsid; 1.
Pfam; PP01543; HCV_capsid; 1.
Pfam; PP01549; HCV_core; 1.
Pfam; PP01559; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; NON TER 414 414
SEQUENCE 414 AA; 45148 MW; D63EE7CED5B71776 CRC64;
                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                 42.9%; Score 82; DB 2; Length 414; 100.0%; Pred. No. 7.5e-72; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 82; Conservative
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us-09-084-691b-206.oli.rai

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Query Match
Best Local Similarity
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US-08-290-665A-206
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CITY: NE
STATE: N
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603.178 Million cell updates/sec
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Sequence 161,
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Sequence 168,
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Sequence 174,
                                                                                                                                                                                                                                       1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-535-866C-228
US-08-290-665A-161
US-08-290-665A-167
US-08-290-665A-174
US-08-290-665A-174
US-08-290-665A-191
US-08-290-665A-191
US-08-290-665A-191
US-08-290-665A-201
US-08-290-665A-201
US-08-290-665A-201
US-08-290-665A-202
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US-08-290-665
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PCT-US95-10398-200
PCT-US95-10398-201
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                                                                                                                                                                                                                                                                                                                                          478139 seqs, 66318000 residues
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                                                                             - protein search, using sw model
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                                                                                                                   October 30, 2004, 01:57:19
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                        score:
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Perfect
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App App	App App App	Appli Appli Appl	Appl App App	App ppli ppli Appli
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Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence
PCT-US95-10398-202 PCT-US95-10398-203 PCT-TE05-10398-203	US-08-635-886C-189 US-08-635-886C-194 US-08-974-690C-189	US-08-974-690C-194 US-09-539-601-3 US-09-539-601-21 US-09-539-601-21	US-09-539-601-33 US-08-290-665A-197 PCT-US95-10398-197 US-08-635-886C-217	US-08-974-690C-217 US-08-905-054B-1 PCT-US92-07813-1 US-07-681-703B-20
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191	4 4 4 0 0 0 0 0	3010 3010 3010	3010 191 191 319	319 75 75 90
26.7	26.7	26.7	26.7 26.2 26.2 26.2	26.2 25.7 25.7 25.7
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28 29	3.5	3.55 3.55 3.65 3.65 5.65 5.65 5.65 5.65	38 39 41 41	24 4 4 4 2 E 4 2

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RESULT 1

RESULT 1

RESULT 1

RESULT 1

SECRETAL SOLUTION:

REPLICANT: BURGA APPLICATION:

RAPLICANT: BURGA A. MILLER, R.H. AND

APPLICANT: BURGA A. MULLER, R.H. AND

APPLICANT: BURGALL, R.H.

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND

TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

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Length 191;

Score 191; DB 2; Pred. No. 1e-173;

100.0%; 100.0%; 0;

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RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                                                                                                          61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRSRNLG 120
                                                                                                                                                                                                                                        APPLICANT: DELEYS, Robert
APPLICANT: MARKIENS, Geert
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
FILE REPERENCE: 2.752-18
FURENT FILING DATE: 1996-04-25
CURRENT FILING DATE: 1996-04-25
PRIOR PELICATION NUMBER: EP 93402718.6
PRIOR PLICATION NUMBER: EP 93402718.6
PRIOR PLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 2.86
SOFTWARE: PACENTIN VERSION 3.1
SOFTWARE: PACENTIN VERSION 3.1
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                                                                                           1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                                 Indels
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100.0%; Pred. No. 1e-173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                 0, Mismatches
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APPLICANT: LEROUX-ROELS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 191, Conservative
                                   191; Conservative
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Matches 191; Conserv
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                                                                                             1 MSTLPKPQRKTKRNTNRRPTDVKRPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                       Gaps
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NUCLEOTIDE AND DEDUCED

NUCLEOTIDE AND DEDUCED

CORE GENES OF THE ENVELOPE 1 AND

CORE GENES OF ISOLATES OF HEPATITIS C VIRUS

AND THE USE OF REAGENTS DERIVED FROM THESE

SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

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                         Indels
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                       0; Mismatches
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APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIFICATION: 15-AUG-1995
CLASSIFICATION: BARD: 08/086,428
FILING DATE: 29 JUNE 1993
FILING DATE: 29 JUNE 1993
FILING DATE: 15-AUG-1993
FILING DATE: 15-AUG-1993
APPLICATION NUMBER: 08/290/665
FILING DATE: 15-AUGUST 1994
ATTORNEY-AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
PCT-US95-10398-206
PCT-US95-10398-206
PCT-US95-10398
PCT-US95-10398
PCT-US95-10398
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HK2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BUKH, J., MIL
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: ANIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: SAND
TITLE OF INVENTION: SEQUENCES: 263
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                           Conservative
                                                                                                                                                                                                                                                                                           181 LLSCLTTPASA 191
                                                                                                                                                                                                                                                                                                                    ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY 1
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Sequence 228, Application US/08974690C
Patent No. 6613333
GENERAL INFORMATION:
APPLICANT: LEROUX-ROBLS, Geert
APPLICANT: DELEYS, Robert
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FINNEGAN
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NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFRENCE/DOCKET NUMBER: 202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
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(212) 758-4800
(212) 751-6849
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TITLE OF INVENTION: CORE GE
TITLE OF INVENTION: CORE GE
TITLE OF INVENTION: CORE GE
TITLE OF INVENTION: SEQUENC
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: homosapiens
; INDIVIDUAL ISOLATE: SA10
US-08-290-665A-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Conservative
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INDIVIDUAL ISOLATE: T
                                                                                                                                                                                                                                                                                                                               unknown
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
NEW YORK
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Best Local Similarity
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    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                      TELEFAX:
TELEX: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: 1
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSTLPKPQRKTKRNTNRRPTDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
            TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C TITLE OF INVENTION: VIRUS FILE REPERENCE: 2551-94 CURRENT APPLICATION NUMBER: US/08/974,690C CURRENT APPLICATION NUMBER: US/08/974,690C CURRENT FILING DATE: 1997-11-19 PRIOR PLLING DATE: 1997-11-19 PRIOR PLLING DATE: 1993-11-04 PRIOR FILING DATE: 1993-11-04 SPRIOR PRIOR PRI
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TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/290,665A
15-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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CRGANISM: hepatitis C virus

US-08-974-690C-228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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Gaps
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                            ;
                                                                                                          21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKISERSQPRGRRQPIPKARQP 71
                                                                                                                                                        21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP
     Length 191;
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                                                         Indels
                                  1.1e-40;
26.7%; Score 51; DB 2;
100.0%; Pred. No. 1.1e-4(
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                     Sequence 167, Application US/08290665A
Patent No. 5882852
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                 AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 26.7%; Score 51; DB 2; L. 1. Similarity 100.0%; Pred. No. 1.1e-40; 51; Conservative 0; Mismatches 0;
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NUCLEOTIDE AND DEDUCED
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                                                                                                                                                                                                                                                                                                                                                                       US/08/290,665A
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665i
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
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GENERAL INFORMATION:
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD INFORMATION:
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
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                                                                                                                MORGAN & FINNEGAN
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TELEX: 421792
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homosapiens INDIVIDUAL ISOLATE: HK3
                                                                                                                                    : 345 PARK AVENUE
NEW YORK
  TITLE OF INVENTION: CORE
TITLE OF INVENTION: SEQUINDERS OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                                                                                                                                                                     ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PURCELL, R
TITLE OF INVENTION: N
TITLE OF INVENTION: A
TITLE OF INVENTION: A
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BUKH, J.,
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Best Local Similarity
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STRANDEDNESS: unb
                                                                                                                                                             CITY: NEW YORK STATE: NEW YORK
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ORIGINAL SOURCE:
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US-08-290-665A-174
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                                                                                                                ADDRESSEE:
STREET: 34
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                                                                                                                                                                                                       COUNTRY:
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ANTHO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 172, Application US/08290665A
Sequence 172, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TILLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DVKFPGGGGIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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                                                     21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                              21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 51; Conservative 0; Mismatches 0; Indels
             Indels
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0
               0; Mismatches
                                                                                                                                                                                                                                                                           MILLER, R.H. AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
COMPATATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2026-4116
                                                                                                                                                                                                            Sequence 168, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 421792
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
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amino acid
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                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCL
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                 51; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                             APPLICANT: BUKH, J., APPLICANT: PURCELL, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
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                 Matches
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STRANDEDNESS: unknown
                            TOPOLOGY: unknown ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                     Query Match
Best Local
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Patent No. 5882852

GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLECTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLARES OF HERATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.7%; Score 51; DB 2; Length 191; ilarity 100.0%; Pred. No. 1.1e-40; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-194
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECHOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                   TELEX: 421792
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 421792
INFORMATION FOR SEQ ID NO: 191:
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NAME: RICHARD W. BORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homosapiens INDIVIDUAL ISOLATE: HK4
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CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown ORIGINAL SOURCE:
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Best Local Similarity
Matches 51; Conserv
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TELEX: 4:
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APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                               Length 191;
                                                                                                                                             0; Indels
                                                                                          ch 26.7%; Score 51; DB 2; Lu Similarity 100.0%; Pred. No. 1.1e-40; 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCEY/DOCKET NUMBER: 36,459
REFERENCEY/DOCKET NUMBER: 36,459
TELECOMMUTCATION INFORMATION:
TELESPHONE: (212) 758-489
                                                                                                                                                                                                                                                                                                                                       US-08-290-665A-198
; Sequence 198, Application US/08290665A
; Patent No. 582885;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORGAN & FINNEGAN
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TELEX.
1192
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homosapiens INDIVIDUAL ISOLATE: SA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 51; Conservative
ORGANISM: homosapiens;
; INDIVIDUAL ISOLATE: Z/
US-08-290-665A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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NEW YORK
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21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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                                                                                                                               COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REGISTRATION NUMBER: 36,259
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1758-4800
                                                                                                                  FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 51; Conservative
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                   NEW YORK
                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                         10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-290-665A-200
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                                            COUNTRY:
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                                       Sequence 199, Application US/08290665A
Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLECTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: AMINO ACID SEQUENCES
TITLE OF INVENTION: AMINO ACID SEQUENCES
TITLE OF INVENTION: SEQUENCES OF ISOLATES OF HERPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.7%; Score 51; DB 2; Lv Best Local Similarity 100.0%; Pred. No. 1.1e-40; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 200, Application US/08290665A Patent No. 5882852 GENERAL INFORMATION: APPLICANT: BUKH, J., MILLER, R.H. AND APPLICANT: PURCELL, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILLING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2026-4116
                                                                                                                                                          TITLE OF INVENTION: NUCLECTIDE AN TITLE OF INVENTION: AMINO ACID SE TITLE OF INVENTION: CORE GENES OF TITLE OF INVENTION: SEQUENCES IN NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGIETRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
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RESULT 12
US-08-290-665A-199
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GENERAL INFORMATION:
APPLICANT: BUDG, J., MILLER, R.H. AND
APPLICANT: BUDG, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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15-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPEY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERREGT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665
                                                                                                                                       Sequence 201, Application US/08290665A
Patent No. 5882852
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                             APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: NUCI
TITLE OF INVENTION: AMIN
TITLE OF INVENTION: CORE
TITLE OF INVENTION: AND
TITLE OF INVENTION: SEQU
NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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US-08-290-665A-202

Sequence 202, Application US/08290665A

Patent No. 5882852

GENERAL INFORMATION:
APPLICANT: BURCH, J., MILLER, R.H. AND
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
CORRESPONDENCE ADDRESS:
ADDRESS AND VACCINES

OF THE OF THE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

OF THE OF THE
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26.7%; Score 51; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 51; Conservative 0; Mismatches 0; Indels
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COMPUTER: FLORPY DISK
COMPUTER: FLORPY DISK
COMPUTER: TEM PC COMPATIBLE
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY, AGENT TYPORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1758-4800
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORGAN & FINNEGAN
                                                                                                                                                      TELEX: 421792
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homosapiens
INDIVIDUAL ISOLATE: SA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 191 amino acids
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ORGANISM: homosapiens
i INDIVIDUAL ISOLATE: SA3
US-08-290-665A-202
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown ORIGINAL SOURCE: ORGANIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: unknown
unknown
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MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: un}
                                                                                                                                                                                                                                                                                                                                       TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-290-665A-201
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        Query Match
        26.74;
        Score 51;
        DB 2;
        Length 191;

        Best Local Similarity 100.04;
        Pred. No. 1.1e-40;
        Antches 51;
        Conservative 0;
        Mismatches 0;
        Indels 0;
        Gaps

        Qy
        21 DVKFPGGGIVGGVYLLPRRGPRIGVRATRKTSERSQPRGRRQPIPKARQP 71
        Db
        21 DVKFPGGGQIVGGVYLLPRRGPRIGVRATRKTSERSQPRGRRQPIPKARQP 71

        Db
        21 DVKFPGGGQIVGGVYLLPRRGPRIGVRATRKTSERSQPRGRRQPIPKARQP 71
        Search completed: October 30, 2004, 02:00:42

        Job time : 21 secs
        21 secs
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Sequence 228, App Sequence 189, App Sequence 194, App Sequence 1, Appli Sequence 217, Appli Sequence 3, Appli Sequence 16, Appli Sequence 192, Appli Se
                                                                                                                                                                                                                                                         October 30, 2004, 01:58:21; Search time 49 Seconds (without alignments) 1263.780 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSTLPKPQRKTKRNTNRRPT......CSFSIFLLALLSCLTTPASA 191
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(gnn2_6')ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(gnn2_6')ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(gnn2_6')ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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(gnn2_6')ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(gnn2_6')ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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(gnn2_6')ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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(gnn2_6')ptodata/1/pubpaa/USO08_DEW_COMB.pep:*
(gnn2_6')ptodata/1/pubpaa/USO08_DEW_COMB.pep:*
(gnn2_6')ptodata/1/pubpaa/USO08_DEW_COMB.pep:*
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(gnn2_6')ptodata/1/pubpaa/USO08_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-651-165-189

US-10-651-165-194

US-10-467-000-1

US-10-467-000-1

US-10-47-000-1

US-09-21-1397-3

US-09-21-1397-3

US-09-891-983A-16

US-09-891-983A-16

US-10-173-480-16

US-10-173-480-16

US-10-173-480-16

US-10-173-10-16

US-10-173-10-16

US-10-18-2910-16
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                                                                                                                                                                               - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-084-691B-206
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                               OM protein
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Sequence 192, App Sequence 8, Appli Sequence 77, Appl Sequence 78, Appl	equence Sequence equence	0 0 0 0	Sequence 166, App Sequence 19, Appl Sequence 6, Appli Sequence 14, Appli	quence 66 quence 8,	9 9 9 9	2007	equence 2, Sequence 2 Sequence 2 Sequence 1	H
US-09-873-224- US-09-756-875-8 US-09-921-397-7 US-09-921-397-77	US-09-851-13 5 US-10-651-1 US-09-306-78	0 US-09-878-10 US-09-878-281-1	4 US-10-268-569-19 US-09-306-780-6 4 US-10-292-129-14	US-09-851-138-66 US-09-306-780-8 0 US-09-899-046-1	0 US-09-899-046-19 0 US-09-878-281-16 0 US-09-878-281-19	0 US-09-873-224-1 0 US-09-873-224-1 US-09-306-780-20	3 US-10-104-966 S US-10-719-619 US-10-268-562	5 US-10-450-649- US-09-306-780-1 0 US-09-194-949- 5 US-10-365-620- 5 US-10-365-620-
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9 25.7 9 25.7 9 25.7 1 25.7	9 25.7 1 9 25.7 1 9 25.7 1	25.7	9 255.7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	25.7	25.7 9 25.7 9 25.7 1	25.7	9 25.7 1	55.7
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ALIGNMENTS

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Sequence 228, Application US/10651165

Publication No. US2004047877A1

GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
APPLICANT: MARKTENS, Geert
TITLE OF INVENTION: UNRUS
TITLE OF INVENTION: UNRUS
TITLE OF INVENTION: UNRUSE: US/10/651,165
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT PILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: PT/FP94/03555
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR PILING DATE: 1994-11-19
PRIOR PILING DATE: 1994-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARR: Patentin version 3.1
SEQ ID NO 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-228
US-10-651-165-228
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Gaps

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APPLICANT: LEROUX-ROBLS, Geert
APPLICANT: DELEYS, Robert
APPLICANT: DELEYS, Robert
TITLE OF INVENTION: IMMUNODMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: UNBURS.
FILE REFERENCE: 2551-94
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/10/651,165
CURRENT APPLICATION NUMBER: US/08/974,690C
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
SUPPRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin Version 3.1
SEQ ID NO 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
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                                                                                                                                                                               21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARQP 71
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: De Francesco, Raffaele
APPLICANT: De Francesco, Giovanni
APPLICANT: Migliaccio, Giovanni
APPLICANT: Paonessa, Giacomo
TITLE OF INVENTION: HERPAITIS C VIRUS REPLICONS
TITLE OF INVENTION: ENPANCED CELLS
FILE REPRESENCE: ITRO003P
CURRENT APPLICATION NUMBER: US/10/467,000
CURRENT PAPLICATION NUMBER: US/10/467,000
PRIOR FILING DATE: 2003-07-21
PRIOR PELICATION NUMBER: 60/263,479
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                   Length 450;
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                                                                                                   0; Indels
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26.7%; Score 51; DB 15; I
Best Local Similarity 100.0%; Pred. No. 2.5e-37;
Matches 51; Conservative 0; Mismatches 0;
                                             26.7%; Score 51; DB 15; I
100.0%; Pred. No. 5.1e-38;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/10467000
; Publication No. US20040067486A1
; GENERAL INFORMATION:
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ORGANISM: hepatitis C virus
                                                                                                   Conservative
                                                   Query Match
Best Local Similarity
Matches 51; Conserv
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US-10-651-165-217
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Sequence 194, Application US/10651165

Publication No. US200400477A1

GENERAL INFORMATION:

APPLICANT: LERCONX-ROBLS, Geert

APPLICANT: DELENOX, Geert

TITLE OF INVENTION: INMUNORMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: URMUNORMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2551-94

CURRENT APPLICATION NUMBER: US/0651,165

CURRENT FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19

PRIOR FILING DATE: 1997-11-19

SPRIOR FILING DATE: 1993-11-04

PRIOR FILING DATE: 1993-11-04

SPRIOR FILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: Patentin version 3.1

SEQ ID NO 194
                                                                                                                                                                                                                                                                                                                                                              Sequence 189, Application US/10651165
| Publication No. US20040047877a1
| GENERAL INCORMATION:
| APPLICANT: LEROUX-ROELS, Geert
| APPLICANT: LEROUX-ROELS, Geert
| APPLICANT: DELEYS, Robert
| TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
| TITLE OF INVENTION: URBER: US/08/51,165
| FILE REPERENCE: 2551.94
| CURRENT APPLICATION NUMBER: US/08/974,690C
| PRIOR APPLICATION NUMBER: US/08/974,690C
| PRIOR APPLICATION NUMBER: EP 93402718.6
| PRIOR FILING DATE: 1994-11-04
| NUMBER OF SEQ ID NOS: 286
| SOFTWARE: Patentin version 3.1
| SSEC ID NO 189
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                                                                                                              61 RRQPIPKARQPQGRHWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPHWGPNDPRRRSRNLG 120
                                                                                121 KVIDTLTCGFADLMGYIPVVGAPLGGVAAALAHGVRAIEDGINYATGNLPGCSFSIFLLA 180
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181 LLSCLTTPASA 191
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ORGANISM:
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Best Local
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Matches

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Gaps

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APPLICANT: HOWARD A. FIELDS AND YURY B. KHUDYAKOV
TITLE OF INVENTION: ANTIGENIC EPITOPES AND MOSAIC POLYPEPTIDES OF HEPATITIS C VIRUS
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: 14114.0349UZ
CURRENT APPLICATION NUMBER: US/09/758,308
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/092,339
PRIOR FILING DATE: 1999-07-10
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APPLICANT: Shah, Dinesh O.
APPLICANT: Shah, Dinesh O.
APPLICANT: Dawson, George A.
APPLICANT: Dawson, George A.
APPLICANT: Dawson, George A.
APPLICANT: Guiterz, Robin A.
APPLICANT: Guiterz, Robin A.
APPLICANT: Desai, Suresh
APPLICANT: Stewart, James D.
TITLE OF INVENTION: Methods For The simultaneous Detection
TITLE OF INVENTION: Methods For The simultaneous Detection
TITLE OF INVENTION: Methods For The simultaneous Detection
TITLE OF INVENTION: Of HCV Antigens And HCV Antibodies
TITLE REFERENCE: 6821.US.01
CURRENT APPLICATION NUMBER: US/09/891,983A
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE : PastSEQ for Windows Version 4.0
LENGTH: 94
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                                                                                                                                                                                                                                                                                                                                                                                               25.7%; Score 49; DB 9;
100.0%; Pred. No. 9e-37;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 16, Application US/09891983A; Publication No. US20030108858A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 16, Application US/10173480; Publication No. US20030152948A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abbott Laboratories
APPLICANT: Shah, Dinesh O.
APPLICANT: Dawson, Greoge A.
APPLICANT: Muerhoff, A. Scott
APPLICANT: Jiang, Lily
APPLICANT: Gutierrez, Robin A.
                                                                                                                                                                                                                                           PatentIn version 3.0
                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-09-758-308-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-09-891-983A-16
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 1
LENGTH: 91
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TITLE OF INVENTION: Method for simultaneously detecting an antigen of, and an antibod
TITLE OF INVENTION: Method for infectious microorganism
FILE REPERENCE: BET 03P0456
CURRENT APPLICATION WUMBER: US/10/431,587
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: FR 0205808
PRIOR APPLICATION NUMBER: FR 0205808
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
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APPLICANT: HYBRIGENICS
TITLE OF INVENTION: SID nucleic acids and polypeptides selected from
TITLE OF INVENTION: Bathogenic strain of the hepatitis C virus and
TITLE OF INVENTION: applications thereof
FILE REPERENCE: B4809A - JAZ
CURRENT PILITIG DATE: 2001-08-02
PRIOR APPLICATION NUMBER: EP 00402225.7
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 25.7%; Score 49; DB 15; Length 75; 1 Similarity 100.0%; Pred. No. 7.7e-37; 49; Conservative 0; Mismatches 0; Indels
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                                           Indels
                       Pred. No. 3.1e-37;
Best Local Similarity 100.0%; Pred. No. 3.1
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; Patent No. US20020090607A1
                                                                                                                                                                                                                                    Sequence 1, Application US/10431587 Publication No. US20040072267A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Hepatitis C virus
US-09-921-397-3
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SEQ ID NO 3
LENGTH: 77
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Best Local Similarity
Matches 49; Conserv
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LENGTH: 75
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Sequence 192, Application US/09899046
Publication No. US20030008274A1
GENERAL INFORMATION:
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US-09-878-281-192
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APPLICANT: Mucrhoff, A. Scott
APPLICANT: Jarag, Lin.
APPLICANT: Jarag, Lin.
APPLICANT: Jarag, Lin.
APPLICANT: Leary, Thomas P.
APPLICANT: Leary, Thomas P.
APPLICANT: Stewart, James L.
APPLICANT: Stewart, James L.
TITLE OF INVENTION: OF HCV ANTIGENS AND HCV ANTIBODIES
FILE REFERENCE: 682.08.P.
TITLE OF INVENTION: OF HCV ANTIGENS AND HCV ANTIBODIES
FILE REFERENCE: 682.08.P.
TITLE OF INVENTION: OF HCV ANTIGENS AND HCV ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/753,910
CURRENT FILING DATE: 2004-01-07
PRIOR APPLICATION NUMBER: US/10/173,480
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-06-26
APPLICANT: Leary, Thomas P.
APPLICANT: Desai, Suresh
APPLICANT: Desai, Suresh
APPLICANT: Desai, Suresh
TITLE OF INVENTION: METHODS FOR THE SIMULTANEOUS DETECTION
TITLE OF INVENTION: OF HCV ANTIGENS AND HCV ANTIBODIES
TITLE OF INVENTION: 02 PLOY ANTIGENS AND HCV ANTIBODIES
TITLE OF INVENTION: 02 PLOY OF THE SIMULTANEOUS DETECTION
CURRENT APPLICATION NUMBER: US/10/173,480
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 94
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Best Local Similarity 100.0%; Pred. No. 9.3e-37;
Matches 49; Conservative 0; Mismatches 0;
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US-10-753-910-16
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040185436A1
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ORGANISM: Artificial Sequence
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Matches 49; Conserv
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US-09-899-046-192
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US-10-753-910-16
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LENGTH: 94
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    New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/899,046 FILING DATE:
PRIOR DELE:
APPLICATION DATA:
APPLICATION NUMBER: 08/362,455
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APPLICATION NUMBER: US/09/878,281
                                                                                                 S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 192, Application US/09878281; Publication No. US20030032005A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/362,455
                                                                                                                                                                                                                                                                                                                                                                                           : 96 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 100.
49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: New TITLE OF INVENTION: Gen. UNDBER OF SEQUENCES: 271 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d)
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-899-046-192
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RESULT 14

US 08/259,721

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APPLICATION NUMBER:
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0
US-09-873-224-192
; Sequence 192, Application US/09873224
; Publication Wo. US20030064360A1
; Publication Wo. US20030064360A1
; GENERAL INFORMATION:
    APPLICANT: «Unknown»
; TITLE OF INVENTION: New sequences of hepatitis C virus
generypes for diagnosis, prophylaxis and therapy.
    NUMBER OF SEQUENCES: 270
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Selease #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/873,224
FILING DATE: 05-Jun-2001
CLASSIFICATION NUMBER: 08/362,455
FILING DATE: -CUNKNOWN>
PRIOR APPLICATION NUMBER: 08/362,455
FILING DATE: -CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
TELEPHONE: O0 32 9 241 07 11
TELEPHONE: 00 32 9 241 07 11
TELEPAX: 00 32 9 241 07 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 DVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKAR
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FATENT NO. US20020150990A1

FAPLICANT: PIKE, IAN

TITLE OF INVENTION: HEPATITIS C VIRUS PEPTIDES
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: Suite 701-E Columbia Square
STREET: 555 13th Street, N. W.

CITY: Washington
STATE: D. C.
COUNTRY: U. S.

ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: IRM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE TO SECURITE SECURITIN SYSTEM: PC-DOS/MS-DOS
SUSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING FILING DATE:
FILING FILING FILING DATE:
FILING FI
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Best Local Similarity 100.0%; Pred. No. 9.5e-37;
Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 192:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 96 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Ghent
COUNTRY: Belgium
ZIP: B-9052
COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-873-224-192
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